

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys	Gly	Asn	Leu	Thr	Gly	Asn	Ser	Lys	Lys	Ala	Ala	Asp	Ser	Gly	Asp	1	5	10	15
Lys	Pro	Val	Ile	Lys	Met	Tyr	Gln	Ile	Gly	Asp	Lys	Pro	Asp	Asn	Leu	20	25	30	
Asp	Glu	Leu	Leu	Ala	Asn	Ala	Asn	Lys	Ile	Ile	Glu	Glu	Lys	Val	Gly	35	40	45	
Ala	Lys	Leu	Asp	Ile	Gln	Tyr	Leu	Gly	Trp	Gly	Asp	Tyr	Gly	Lys	Lys	50	55	60	
Met	Ser	Val	Ile	Thr	Ser	Ser	Gly	Glu	Asn	Tyr	Asp	Ile	Ala	Phe	Ala	65	70	75	80
Asp	Asn	Tyr	Ile	Val	Asn	Ala	Gln	Lys	Gly	Ala	Tyr	Ala	Asp	Leu	Thr	85	90	95	
Glu	Leu	Tyr	Lys	Lys	Glu	Gly	Lys	Asp	Leu	Tyr	Lys	Ala	Leu	Asp	Pro	100	105	110	
Ala	Tyr	Ile	Lys	Gly	Asn	Thr	Val	Asn	Gly	Lys	Ile	Tyr	Ala	Val	Pro	115	120	125	
Val	Ala	Ala	Asn	Val	Ala	Ser	Gln	Asn	Phe	Ala	Phe	Asn	Gly	Thr	130	135	140		
Leu	Leu	Ala	Lys	Tyr	Gly	Ile	Asp	Ile	Ser	Gly	Val	Thr	Ser	Tyr	Glu	145	150	155	160
Thr	Leu	Glu	Pro	Val	Leu	Lys	Gln	Ile	Lys	Glu	Lys	Ala	Pro	Asp	Val	165	170	175	
Val	Pro	Phe	Ala	Ile	Gly	Lys	Val	Phe	Ile	Pro	Ser	Asp	Asn	Phe	Asp	180	185	190	
Tyr	Pro	Val	Ala	Asn	Gly	Leu	Pro	Phe	Val	Ile	Asp	Leu	Glu	Gly	Asp	195	200	205	
Thr	Thr	Lys	Val	Val	Asn	Arg	Tyr	Glu	Val	Pro	Arg	Phe	Lys	Glu	His	210	215	220	
Leu	Lys	Thr	Leu	His	Lys	Phe	Tyr	Glu	Ala	Gly	Tyr	Ile	Pro	Lys	Asp	225	230	235	240
Val	Ala	Thr	Ser	Asp	Thr	Ser	Phe	Asp	Leu	Gln	Gln	Asp	Thr	Trp	Phe	245	250	255	
Val	Arg	Glu	Glu	Thr	Val	Gly	Pro	Ala	Asp	Tyr	Gly	Asn	Ser	Leu	Leu	260	265	270	
Ser	Arg	Val	Ala	Asn	Lys	Asp	Ile	Gln	Ile	Lys	Pro	Ile	Thr	Asn	Phe	275	280	285	
Ile	Lys	Xaa	Asn	Gln	Thr	Thr	Gln	Val	Ala	Asn	Phe	Val	Ile	Ser	Asn	290	295	300	
Asn	Ser	Lys	Asn	Lys	Glu	Lys	Ser	Met	Glu	Ile	Leu	Asn	Leu	Leu	Asn	305	310	315	320
Thr	Asn	Pro	Glu	Leu	Leu	Asn	Gly	Leu	Val	Tyr	Gly	Pro	Glu	Gly	Lys				

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325

330

335

Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp
 340 345 350

Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn
 355 360 365

Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn
 370 375 380

Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe
 385 390 395 400

Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn
 405 410 415

Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro
 420 425 430

Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala
 435 440 445

Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu
 450 455 460

Lys Asn Lys Lys
 465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTGGTATATC AACGGAAAGG CACCATTTCG AGTGTATTTT CAAGACTACA TGGCTAAGAA	240
ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGGTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAAGTTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAAC TCAACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

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TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840
 CGCAGCTCGC TGGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gln	Gly	Thr	Ala	Ser	Lys	Asp	Asn	Lys	Glu	Ala	Glu	Leu	Lys	Lys	1	5	10	15
Val	Asp	Phe	Ile	Leu	Asp	Trp	Thr	Pro	Asn	Thr	Asn	His	Thr	Gly	Leu	20	25	30	
Tyr	Val	Ala	Lys	Glu	Lys	Gly	Tyr	Phe	Lys	Glu	Ala	Gly	Val	Asp	Val	35	40	45	
Asp	Leu	Lys	Leu	Pro	Pro	Glu	Glu	Ser	Ser	Ser	Asp	Leu	Val	Ile	Asn	50	55	60	
Gly	Lys	Ala	Pro	Phe	Ala	Val	Tyr	Phe	Gln	Asp	Tyr	Met	Ala	Lys	Lys	65	70	75	80
Leu	Glu	Lys	Gly	Ala	Gly	Ile	Thr	Ala	Val	Ala	Ala	Ile	Val	Glu	His	85	90	95	
Asn	Thr	Ser	Gly	Ile	Ile	Ser	Arg	Lys	Ser	Asp	Asn	Val	Ser	Ser	Pro	100	105	110	
Lys	Asp	Leu	Val	Gly	Lys	Lys	Tyr	Gly	Thr	Trp	Asn	Asp	Pro	Thr	Glu	115	120	125	
Leu	Ala	Met	Leu	Lys	Thr	Leu	Val	Glu	Ser	Gln	Gly	Gly	Asp	Phe	Glu	130	135	140	
Lys	Val	Glu	Lys	Val	Pro	Asn	Asn	Asp	Ser	Asn	Ser	Ile	Thr	Pro	Ile	145	150	155	160
Ala	Asn	Gly	Val	Phe	Asp	Thr	Ala	Trp	Ile	Tyr	Tyr	Gly	Trp	Asp	Gly	165	170	175	
Ile	Leu	Ala	Lys	Ser	Gln	Gly	Val	Asp	Ala	Asn	Phe	Met	Tyr	Leu	Lys	180	185	190	
Asp	Tyr	Val	Lys	Glu	Phe	Asp	Tyr	Tyr	Ser	Pro	Val	Ile	Ile	Ala	Asn	195	200	205	
Asn	Asp	Tyr	Leu	Lys	Asp	Asn	Lys	Glu	Glu	Ala	Arg	Lys	Val	Ile	Gln	210	215	220	

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Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala
 225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp
 245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp
 260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr
 275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys
 290 295 300

Gly Phe Thr Asn Glu Phe Val Lys
 305 310

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAAGCG GTGAACTGCG AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTTAA ATACATTTCA GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC	360
ACCTAAGACT GGTCTCATTA CAGACGTCAA ACAACTTGAA GGTAAAACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGA CTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Ser	Gly	Gly	Asn	Ala	Gly	Ser	Ser	Ser	Gly	Lys	Thr	Thr	Ala	Lys	1	5	10	15
Ala	Arg	Thr	Ile	Asp	Glu	Ile	Lys	Lys	Ser	Gly	Glu	Leu	Arg	Ile	Ala	20	25	30	
Val	Phe	Gly	Asp	Lys	Lys	Pro	Phe	Gly	Tyr	Val	Asp	Asn	Asp	Gly	Ser	35	40	45	
Thr	Lys	Val	Arg	Tyr	Asp	Ile	Glu	Leu	Gly	Asn	Gln	Leu	Ala	Gln	Asp	50	55	60	
Leu	Gly	Val	Lys	Val	Lys	Tyr	Ile	Ser	Val	Asp	Ala	Ala	Asn	Arg	Ala	65	70	75	80
Glu	Tyr	Leu	Ile	Ser	Asn	Lys	Val	Asp	Ile	Thr	Leu	Ala	Asn	Phe	Thr	85	90	95	
Val	Thr	Asp	Glu	Arg	Lys	Lys	Gln	Val	Asp	Phe	Ala	Leu	Pro	Tyr	Met	100	105	110	
Lys	Val	Ser	Leu	Gly	Val	Val	Ser	Pro	Lys	Thr	Gly	Leu	Ile	Thr	Asp	115	120	125	
Val	Lys	Gln	Leu	Glu	Gly	Lys	Thr	Leu	Ile	Val	Thr	Lys	Gly	Thr	Thr	130	135	140	
Ala	Glu	Thr	Tyr	Phe	Glu	Lys	Asn	His	Pro	Glu	Ile	Lys	Leu	Gln	Lys	145	150	155	160
Tyr	Asp	Gln	Tyr	Ser	Asp	Ser	Tyr	Gln	Ala	Leu	Leu	Asp	Gly	Arg	Gly	165	170	175	
Asp	Ala	Phe	Ser	Thr	Asp	Asn	Thr	Glu	Val	Leu	Ala	Trp	Ala	Leu	Glu	180	185	190	
Asn	Lys	Gly	Phe	Glu	Val	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Pro	Asp	Thr	195	200	205	
Ile	Ala	Ala	Ala	Val	Gln	Lys	Gly	Asn	Gln	Glu	Leu	Leu	Asp	Phe	Ile	210	215	220	
Asn	Lys	Asp	Ile	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Phe	Phe	His	Lys	Ala	225	230	235	240
Tyr	Glu	Lys	Thr	Leu	His	Pro	Thr	Tyr	Gly	Asp	Ala	Ala	Lys	Ala	Asp	245	250	255	
Asp	Leu	Val	Val	Glu	Gly	Gly	Lys	Val	Asp							260	265		

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAACATAT GGTAAATCTG CGGATGGCAC AGTGACCATC GAGTATTTCA ACCAGAAAAA	60
AGAAATGACC AAAACCTTGG AAGAAATCAC TCGTGATTTT GAGAAGGAAA ACCCTAAGAT	120
CAAGGTCAAA GTCGTCAATG TACCAAATGC TGGTGAAGTA TTGAAGACAC GCGTTCTCGC	180
AGGAGATGTG CCTGATGTGG TCAATATTTA CCCACAGTCC ATCGAACTGC AAGAATGGGC	240
AAAAGCAGGT GTTTTTGAAG ATTTGAGCAA CAAAGACTAC CTGAAACGCG TGAAAAATGG	300
CTACGCTGAA AAATATGCTG TAAACGAAAA AGTTTACAAC GTTCCTTTTA CAGCTAATGC	360
TTATGGAATT TACTACAACA AAGATAAATT CGAAGAAGT GGCCTGAAGG TTCCTGAAAC	420
CTGGGATGAA TTTGAACAGT TAGTCAAAGA TATCGTTGCT AAAGGACAAA CACCATTTGG	480
AATTGCAGGT GCAGATGCTT GGACACTCAA TGGTTACAAT CAATTAGCCT TTGCGACAGC	540
AACAGGTGGA GGAAAAGAAG CAAATCAATA CCTTCGTTAT TCTCAACCAA ATGCCATTAA	600
ATTGTCGGAT CCGATTATGA AAGATGATAT CAAGGTCATG GACATCCTTC GCATCAATGG	660
ATCTAAGCAA AAGAACTGGG AAGGTGCTGG CTATACCGAT GTTATCGGAG CCTTCGCACG	720
TGGGGATGTC CTCATGACAC CAAATGGGTC TTGGGCGATC ACAGCGATTA ATGAACAAAA	780
ACCGAAGCTT AAGATTGGGA CCTTCATGAT TCCAGGAAAA GAAAAAGGAC AAAGCTTAAC	840
CGTTGGTGCG GGAGACTTGG CATGGTCTAT CTCAGCCACC ACCAAACATC CAAAAGAAGC	900
CAATGCCTTT GTGGAATATA TGACCCGTCC AGAAGTCATG CAAAAATACT ACGATGTGGA	960
CGGATCTCCA ACAGCGATCG AAGGGGTCAA ACAAGCAGGA GAAGATTAC CGCTTGCTGG	1020
TATGACCGAA TATGCCTTTA CGGATCGTCA CTTGGTCTGG TTGCAACAAT ACTGGACCAG	1080
TGAAGCAGAC TTCCATACCT TGACCATGAA CTATGTCTTG ACCGGTGATA AACAAGGCAT	1140
GGTCAATGAT TTGAATGCCT TCTTTAACCC GATGAAAGCG GATGTGGAT	1189

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5					10					15	

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Asn Gln Lys Lys Glu Met Thr Lys Thr Leu Glu Glu Ile Thr Arg Asp
 20 25 30
 Phe Glu Lys Glu Asn Pro Lys Ile Lys Val Lys Val Val Asn Val Pro
 35 40 45
 Asn Ala Gly Glu Val Leu Lys Thr Arg Val Leu Ala Gly Asp Val Pro
 50 55 60
 Asp Val Val Asn Ile Tyr Pro Gln Ser Ile Glu Leu Gln Glu Trp Ala
 65 70 75 80
 Lys Ala Gly Val Phe Glu Asp Leu Ser Asn Lys Asp Tyr Leu Lys Arg
 85 90 95
 Val Lys Asn Gly Tyr Ala Glu Lys Tyr Ala Val Asn Glu Lys Val Tyr
 100 105 110
 Asn Val Pro Phe Thr Ala Asn Ala Tyr Gly Ile Tyr Tyr Asn Lys Asp
 115 120 125
 Lys Phe Glu Glu Leu Gly Leu Lys Val Pro Glu Thr Trp Asp Glu Phe
 130 135 140
 Glu Gln Leu Val Lys Asp Ile Val Ala Lys Gly Gln Thr Pro Phe Gly
 145 150 155 160
 Ile Ala Gly Ala Asp Ala Trp Thr Leu Asn Gly Tyr Asn Gln Leu Ala
 165 170 175
 Phe Ala Thr Ala Thr Gly Gly Gly Lys Glu Ala Asn Gln Tyr Leu Arg
 180 185 190
 Tyr Ser Gln Pro Asn Ala Ile Lys Leu Ser Asp Pro Ile Met Lys Asp
 195 200 205
 Asp Ile Lys Val Met Asp Ile Leu Arg Ile Asn Gly Ser Lys Gln Lys
 210 215 220
 Asn Trp Glu Gly Ala Gly Tyr Thr Asp Val Ile Gly Ala Phe Ala Arg
 225 230 235 240
 Gly Asp Val Leu Met Thr Pro Asn Gly Ser Trp Ala Ile Thr Ala Ile
 245 250 255
 Asn Glu Gln Lys Pro Asn Phe Lys Ile Gly Thr Phe Met Ile Pro Gly
 260 265 270
 Lys Glu Lys Gly Gln Ser Leu Thr Val Gly Ala Gly Asp Leu Ala Trp
 275 280 285
 Ser Ile Ser Ala Thr Thr Lys His Pro Lys Glu Ala Asn Ala Phe Val
 290 295 300
 Glu Tyr Met Thr Arg Pro Glu Val Met Gln Lys Tyr Tyr Asp Val Asp
 305 310 315 320
 Gly Ser Pro Thr Ala Ile Glu Gly Val Lys Gln Ala Gly Glu Asp Ser
 325 330 335
 Pro Leu Ala Gly Met Thr Glu Tyr Ala Phe Thr Asp Arg His Leu Val
 340 345 350

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Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp
385 390 395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGGGAAAAAT	TCTAGCGAAA	CTAGTGGAGA	TAATTGGTCA	AAGTACCACT	CTAACAAGTC	60
TATTACTATT	GGATTTGATA	GTACTTTTGT	TCCAATGGGA	TTTGCTCAGA	AAGATGGTTC	120
TTATGCAGGA	TTTGATATTG	ATTTAGCTAC	AGCTGTTTTT	GAAAAATACG	GAATCACGGT	180
AAATTGGCAA	CCGATTGATT	GGGATTTGAA	AGAAGCTGAA	TTGACAAAAG	GAACGATTGA	240
TCTGATTTGG	AATGGCTATT	CCGCTACAGA	CGAACGCCGT	GAAAAGGTGG	CTTTCAGTAA	300
CTCATATATG	AAGAATGAGC	AGGTATTGGT	TACGAAGAAA	TCATCTGGTA	TCACGACTGC	360
AAAGGATATG	ACTGGAAAGA	CATTAGGAGC	TCAAGCTGGT	TCATCTGGTT	ATGCGGACTT	420
TGAAGCAAAT	CCAGAAATTT	TGAAGAATAT	TGTCGCTAAT	AAGGAAGCGA	ATCAATACCA	480
AACCTTTAAT	GAAGCCTTGA	TTGATTTGAA	AAACGATCGA	ATTGATGGTC	TATTGATTGA	540
CCGTGTCTAT	GCAAACTATT	ATTTAGAAGC	AGAAGGTGTT	TTAAACGATT	ATAATGTCTT	600
TACAGTTGGA	CTAGAAACAG	AAGCTTTTGC	GGTTGGAGCC	CGTAAGGAAG	ATACAAACTT	660
GGTTAAGAAG	ATAAATGAAG	CTTTTCTAG	TCTTTACAAG	GACGGCAAGT	TCCAAGAAAT	720
CAGCCAAAAA	TGGTTTGGAG	AAGATGTAGC	AACCAAAGAA	GTAAAAAGAAG	GACAG	775

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met

131

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Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu
35 40 45

Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro
50 55 60

Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp
65 70 75 80

Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val
85 90 95

Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys
100 105 110

Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu
115 120 125

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro
130 135 140

Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln
145 150 155 160

Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly
165 170 175

Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly
180 185 190

Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala
195 200 205

Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile
210 215 220

Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile
225 230 235 240

Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu
245 250 255

Gly Gln

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 868 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAACTC 60
 AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT 120

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TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT 240
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420
 CAAAGACCTT AACAATAAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480
 AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAACTCCT GAACAAATCA AGACCTTGGT 660
 TGAAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAAA TCTTTACTGA 780
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val
 1 5 10 15
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp
 20 25 30
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu
 35 40 45
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu
 50 55 60
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe
 65 70 75 80
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe
 85 90 95
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu
 100 105 110
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile
 115 120 125

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn
 130 135 140
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu
 145 150 155 160
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala
 165 170 175
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser
 180 185 190
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu
 195 200 205
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg
 210 215 220
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg
 225 230 235 240
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln
 245 250 255
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr
 260 265 270
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala
 275 280 285
 Lys

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGA GAAGGAAACT GCGGTTTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTACTGATGA	540

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA 600
 TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC 660
 TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA 720
 CTTACACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA 780
 AAAAGGCCTG ATTGATAAAG AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG 840
 TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA 900
 CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG 960
 TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT 1020
 AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA 1080
 CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA 1140
 TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA 1200
 AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA 1260
 TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT 1320
 CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTG GACAAGATTG CCCATATCGA 1380
 AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT 1440
 TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT 1500
 CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC 1546

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
 1 5 10 15

Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
 20 25 30

Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
 35 40 45

Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
 50 55 60

Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
 65 70 75 80

Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

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				85					90					95	
Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr
			100					105					110		
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala
		115					120					125			
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu
	130					135					140				
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala
145					150					155					160
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys
			165						170					175	
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp
		180						185					190		
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser
		195					200					205			
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile
	210					215					220				
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp
225					230					235					240
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg
			245						250					255	
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp
		260						265					270		
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr
		275				280						285			
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp
	290					295					300				
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg
305					310					315					320
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val
			325						330					335	
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala
			340					345					350		
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys
		355					360					365			
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His
	370					375					380				
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu
385					390					395					400
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr
			405						410					415	
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr

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420

425

430

Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met
435 440 445

Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn
450 455 460

Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile
465 470 475 480

Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu
485 490 495

Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala
500 505 510

Asn Lys Asn
515

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAAGT TCACTGGACG AGGTCAAACCT TTCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO:24:

096527 0430
102210 2259460

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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Ser Thr Asn Ser Ser Thr Ser Gln Thr Glu Thr Ser Ser Ser Ala Pro
1          5          10          15

Thr Glu Val Thr Ile Lys Ser Ser Leu Asp Glu Val Lys Leu Ser Lys
          20          25          30

Val Pro Glu Lys Ile Val Thr Phe Asp Leu Gly Ala Ala Asp Thr Ile
          35          40          45

Arg Ala Leu Gly Phe Glu Lys Asn Ile Val Gly Met Pro Thr Lys Thr
          50          55          60

Val Pro Thr Tyr Leu Lys Asp Leu Val Gly Thr Val Lys Asn Val Gly
          65          70          75          80

Ser Met Lys Glu Pro Asp Leu Glu Ala Ile Ala Ala Leu Glu Pro Asp
          85          90          95

Leu Ile Ile Ala Ser Pro Arg Thr Gln Lys Phe Val Asp Lys Phe Lys
          100          105          110

Glu Ile Ala Pro Thr Val Leu Phe Gln Ala Ser Lys Asp Asp Tyr Trp
          115          120          125

Thr Ser Thr Lys Ala Asn Ile Glu Ser Leu Ala Ser Ala Phe Gly Glu
          130          135          140

Thr Gly Thr Gln Lys Ala Lys Glu Glu Leu Thr Lys Leu Asp Lys Ser
          145          150          155          160

Ile Gln Glu Val Ala Thr Lys Asn Glu Ser Ser Asp Lys Lys Ala Leu
          165          170          175

Ala Ile Leu Leu Asn Glu Gly Lys Met Ala Ala Phe Gly Ala Lys Ser
          180          185          190

Arg Phe Ser Phe Leu Tyr Gln Thr Leu Lys Phe Lys Pro Thr Asp Thr
          195          200          205

Lys Phe Glu Asp Ser Arg His Gly Gln Glu Val Ser Phe Glu Ser Val
          210          215          220

Lys Glu Ile Asn Pro Asp Ile Leu Phe Val Ile Asn Arg Thr Leu Ala
          225          230          235          240

Ile Gly Gly Asp Asn Ser Ser Asn Asp Gly Val Leu Glu Asn Ala Leu
          245          250          255

Ile Ala Glu Thr Pro Ala Ala Lys Asn Gly Lys Ile Ile Gln Leu Thr
          260          265          270

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Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT	GGCGGAAGTA	AAGATGCTGC	CAAATCAGGT	GGTGACGGTG	CCAAAACAGA	60
AATCACTTGG	TGGGCATTCC	CAGTATTTAC	CCAAGAAAAA	ACTGGTGACG	GTGTTGGAAC	120
TTATGAAAAA	TCAATCATCG	AAGCGTTTGA	AAAAGCAAAC	CCAGATATAA	AAGTGAAATT	180
GGAAACCATC	GACTTCAAGT	CAGGTCCTGA	AAAAATCACA	ACAGCCATCG	AAGCAGGAAC	240
AGCTCCAGAC	GTACTCTTTG	ATGCACCAGG	ACGTATCATC	CAATACGGTA	AAAACGGTAA	300
ATTGGCTGAG	TTGAATGACC	TCTTCACAGA	TGAATTTGTT	AAAGATGTCA	ACAATGAAAA	360
CATCGTACAA	GCAAGTAAAG	CTGGAGACAA	GGCTTATATG	TATCCGATTA	GTTCTGCCCC	420
ATTCTACATG	GCAATGAACA	AGAAAATGTT	AGAAGATGCT	GGAGTAGCAA	ACCTTGTAAG	480
AGAAGGTTGG	ACAAGTATG	ATTTTGAAAA	AGTATTGAAA	GCACTTAAAG	ACAAGGGTTA	540
CACACCAGGT	TCATTGTTCA	GTTCTGGTCA	AGGGGGAGAC	CAAGGAACAC	GTGCCTTTAT	600
CTCTAACCTT	TATAGCGGTT	CTGTAACAGA	TGAAAAAGTT	AGCAAATATA	CAACTGATGA	660
TCCTAAATTC	GTCAAAGGTC	TTGAAAAAGC	AACTAGCTGG	ATTAAAGACA	ATTTGATCAA	720
TAATGGTTCA	CAATTTGACG	GTGGGGCAGA	TATCCAAAAC	TTTGCCAACG	GTCAAACATC	780
TTACACAATC	CTTTGGGCAC	CAGCTCAAAA	TGGTATCCAA	GCTAAACTTT	TAGAAGCAAG	840
TAAGGTAGAA	GTGGTAGAAG	TACCATTCCC	ATCAGACGAA	GGTAAGCCAG	CTCTTGAGTA	900
CCTTGTA AAC	GGGTTTGCAG	TATTCAACAA	TAAAGACGAC	AAGAAAGTCG	CTGCATCTAA	960
GAAATTCATC	CAGTTTATCG	CAGATGACAA	GGAGTGGGGA	CCTAAAGACG	TAGTTCGTAC	1020
AGGTGCTTTC	CCAGTCCGTA	CTTCATTTGG	AAAACTTTAT	GAAGACAAAC	GCATGGAAAC	1080
AATCAGCGGC	TGGACTCAAT	ACTACTCACC	ATACTACAAC	ACTATTGATG	GATTTGCTGA	1140
AATGAGAACA	CTTTGGTTCC	CAATGTTGCA	ATCTGTATCA	AATGGTGACG	AAAAACCAGC	1200
AGATGCTTTG	AAAGCCTTCA	CTGAAAAAGC	GAACGAAACA	ATCAAAAAAG	CTATGAAACA	1260
A						1261

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala Lys Ser Gly Gly Asp Gly
1           5           10           15
Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe Pro Val Phe Thr Gln Glu
20           25           30
Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu Lys Ser Ile Ile Glu Ala
35           40           45
Phe Glu Lys Ala Asn Pro Asp Ile Lys Val Lys Leu Glu Thr Ile Asp
50           55           60
Phe Lys Ser Gly Pro Glu Lys Ile Thr Thr Ala Ile Glu Ala Gly Thr
65           70           75           80
Ala Pro Asp Val Leu Phe Asp Ala Pro Gly Arg Ile Ile Gln Tyr Gly
85           90           95
Lys Asn Gly Lys Leu Ala Glu Leu Asn Asp Leu Phe Thr Asp Glu Phe
100          105          110
Val Lys Asp Val Asn Asn Glu Asn Ile Val Gln Ala Ser Lys Ala Gly
115          120          125
Asp Lys Ala Tyr Met Tyr Pro Ile Ser Ser Ala Pro Phe Tyr Met Ala
130          135          140
Met Asn Lys Lys Met Leu Glu Asp Ala Gly Val Ala Asn Leu Val Lys
145          150          155          160
Glu Gly Trp Thr Thr Asp Asp Phe Glu Lys Val Leu Lys Ala Leu Lys
165          170          175
Asp Lys Gly Tyr Thr Pro Gly Ser Leu Phe Ser Ser Gly Gln Gly Gly
180          185          190
Asp Gln Gly Thr Arg Ala Phe Ile Ser Asn Leu Tyr Ser Gly Ser Val
195          200          205
Thr Asp Glu Lys Val Ser Lys Tyr Thr Thr Asp Asp Pro Lys Phe Val
210          215          220
Lys Gly Leu Glu Lys Ala Thr Ser Trp Ile Lys Asp Asn Leu Ile Asn
225          230          235          240
Asn Gly Ser Gln Phe Asp Gly Gly Ala Asp Ile Gln Asn Phe Ala Asn
245          250          255
Gly Gln Thr Ser Tyr Thr Ile Leu Trp Ala Pro Ala Gln Asn Gly Ile
260          265          270

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Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro
 275 280 285
 Phe Pro Ser Asp Glu Gly Lys Pro Ala Leu Glu Tyr Leu Val Asn Gly
 290 295 300
 Phe Ala Val Phe Asn Asn Lys Asp Asp Lys Lys Val Ala Ala Ser Lys
 305 310 315 320
 Lys Phe Ile Gln Phe Ile Ala Asp Asp Lys Glu Trp Gly Pro Lys Asp
 325 330 335
 Val Val Arg Thr Gly Ala Phe Pro Val Arg Thr Ser Phe Gly Lys Leu
 340 345 350
 Tyr Glu Asp Lys Arg Met Glu Thr Ile Ser Gly Trp Thr Gln Tyr Tyr
 355 360 365
 Ser Pro Tyr Tyr Asn Thr Ile Asp Gly Phe Ala Glu Met Arg Thr Leu
 370 375 380
 Trp Phe Pro Met Leu Gln Ser Val Ser Asn Gly Asp Glu Lys Pro Ala
 385 390 395 400
 Asp Ala Leu Lys Ala Phe Thr Glu Lys Ala Asn Glu Thr Ile Lys Lys
 405 410 415
 Ala Met Lys Gln
 420

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAAA ATGAAGATGG AGAAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAATCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT	658

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
 1 5 10 15
 Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
 20 25 30
 Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
 35 40 45
 Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
 50 55 60
 Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
 65 70 75 80
 Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
 85 90 95
 Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
 100 105 110
 Tyr Val Asn Gln Asp Gly Lys Ala Ala Ala Asp Arg Tyr Ser Ala Arg
 115 120 125
 Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
 130 135 140
 Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
 145 150 155 160
 Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
 165 170 175
 Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
 180 185 190
 Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
 195 200 205
 Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
 210 215

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG 120
GAAATCAACA CTCATTAAAA CCTTGCTCTG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480
ACTTTTAGAT GAGCCAACTA CTTACTTGA TATCTCATAT CAAATAGAAC TATTAGACCT 540
CTTGACTGAT CTAAACCAAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780
TGTTAECTCT 790

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile
1 5 10 15
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val
20 25 30
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu
35 40 45
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys
50 55 60
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile
65 70 75 80
Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu
85 90 95

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T0229 2259/60

Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly
 100 105 110
 Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val
 115 120 125
 Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg
 130 135 140
 Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu
 145 150 155 160
 Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu
 165 170 175
 Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile
 180 185 190
 Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr
 195 200 205
 Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu
 210 215 220
 Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala
 225 230 235 240
 Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile
 245 250 255
 Gly Lys His His Val Ser
 260

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACCTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG 60
 CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC 120
 CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA 180
 AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG 240
 AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT 300
 GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC 360
 TGTACCGAAT GACGCTACAA ACGAAAGCCG TCGCTTTTAT TTGCTTCAAT CAGCTGGCTT 420
 GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC 480
 AAAGAAGTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT 540

TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600
 ACTTTTCAAA GAACAAGCTG ATGAAAATC AAAACAATGG TACAACATCA TTGTTGCAAA 660
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG 780
 G 781

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Ser Glu Lys Lys Ala Asp Asn Ala Thr Thr Ile Lys Ile Ala Thr
 1 5 10 15
 Val Asn Arg Ser Gly Ser Glu Glu Lys Arg Trp Asp Lys Ile Gln Glu
 20 25 30
 Leu Val Lys Lys Asp Gly Ile Thr Leu Glu Phe Thr Glu Phe Thr Asp
 35 40 45
 Tyr Ser Gln Pro Asn Lys Ala Thr Ala Asp Gly Glu Val Asp Leu Asn
 50 55 60
 Ala Phe Gln His Tyr Asn Phe Leu Asn Asn Trp Asn Lys Glu Asn Gly
 65 70 75 80
 Lys Asp Leu Val Ala Ile Ala Asp Thr Tyr Ile Ser Pro Ile Arg Leu
 85 90 95
 Tyr Ser Gly Leu Asn Gly Ser Ala Asn Lys Tyr Thr Lys Val Glu Asp
 100 105 110
 Ile Pro Ala Asn Gly Glu Ile Ala Val Pro Asn Asp Ala Thr Asn Glu
 115 120 125
 Ser Arg Ala Leu Tyr Leu Leu Gln Ser Ala Gly Leu Ile Lys Leu Asp
 130 135 140
 Val Ser Gly Thr Ala Leu Ala Thr Val Ala Asn Ile Lys Glu Asn Pro
 145 150 155 160
 Lys Asn Leu Lys Ile Thr Glu Leu Asp Ala Ser Gln Thr Ala Arg Ser
 165 170 175
 Leu Ser Ser Val Asp Ala Ala Val Val Asn Asn Thr Phe Val Thr Glu
 180 185 190
 Ala Lys Leu Asp Tyr Lys Lys Ser Leu Phe Lys Glu Gln Ala Asp Glu
 195 200 205

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Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu
 210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His
 225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp
 245 250 255

Gln Pro Val Trp
 260

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTCTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val
 1 5 10 15

Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala

146

20

25

30

Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln
35 40 45

Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu
50 55 60

Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala
65 70 75 80

Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu
85 90 95

Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu
100 105 110

Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln
115 120 125

Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys
130 135 140

Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser
145 150 155 160

Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser
165 170 175

Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala
180 185 190

Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly
195 200 205

Thr Pro Ser Leu Gln
210

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC	60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTCACTG	120
TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAACT AAAGCTACGG TTGTAGAAAA	180
ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG AATCTAATGG	240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA	300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG	360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG	420

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(2) INFORMATION FOR SEQ ID NO:36:

(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTA AAAAAGC	420
GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720
AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACTGT	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

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(ii) MOLECULE TYPE: protein

Asp	Glu	Gln	Lys	Ile	Lys	Gln	Ala	Glu	Ala	Glu	Val	Glu	Ser	Lys	Gln	
1				5				10						15		
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Lys	Ile	Lys	Thr	Asp	Arg	Glu	Glu	Ala	
			20					25					30			
Glu	Glu	Glu	Ala	Lys	Arg	Arg	Ala	Asp	Ala	Lys	Glu	Gln	Gly	Lys	Pro	
		35					40					45				
Lys	Gly	Arg	Ala	Lys	Arg	Gly	Val	Pro	Gly	Glu	Leu	Ala	Thr	Pro	Asp	
	50					55					60					
Lys	Lys	Glu	Asn	Asp	Ala	Lys	Ser	Ser	Asp	Ser	Ser	Val	Gly	Glu	Glu	
65					70					75					80	
Thr	Leu	Pro	Ser	Pro	Ser	Leu	Lys	Pro	Glu	Lys	Lys	Val	Ala	Glu	Ala	
			85						90					95		
Glu	Lys	Lys	Val	Glu	Glu	Ala	Lys	Lys	Lys	Ala	Glu	Asp	Gln	Lys	Glu	
			100					105					110			
Glu	Asp	Arg	Arg	Asn	Tyr	Pro	Thr	Asn	Thr	Tyr	Lys	Thr	Leu	Glu	Leu	
		115					120					125				
Glu	Ile	Ala	Glu	Ser	Asp	Val	Glu	Val	Lys	Lys	Ala	Glu	Leu	Glu	Leu	
	130					135					140					
Val	Lys	Glu	Glu	Ala	Lys	Glu	Pro	Arg	Asn	Glu	Glu	Lys	Val	Lys	Gln	
145					150					155					160	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Lys	Lys	Ala	Glu	Ala	Thr	Arg	Leu	Glu	
				165					170					175		
Lys	Ile	Lys	Thr	Asp	Arg	Lys	Lys	Ala	Glu	Glu	Glu	Ala	Lys	Arg	Lys	
			180					185					190			
Ala	Ala	Glu	Glu	Asp	Lys	Val	Lys	Glu	Lys	Pro	Ala	Glu	Gln	Pro	Gln	
		195					200					205				
Pro	Ala	Pro	Ala	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Lys	Pro	
	210					215					220					
Glu	Asn	Pro	Ala	Glu	Gln	Pro	Lys	Ala	Glu	Lys	Pro	Ala	Asp	Gln	Gln	
225					230					235					240	
Ala	Glu	Glu	Asp	Tyr	Ala	Arg	Arg	Ser	Glu	Glu	Glu	Tyr	Asn	Arg	Leu	
				245					250					255		
Thr	Gln	Gln	Gln	Pro	Pro	Lys	Thr	Glu	Lys	Pro	Ala	Gln	Pro	Ser	Thr	
			260					265					270			
Pro	Lys	Thr	Gly	Trp	Lys	Gln	Glu	Asn	Gly	Met	Trp	Tyr	Phe	Tyr	Asn	
		275					280					285				

150

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp
290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn
305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser
340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp
370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp
385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser
405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly
420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn
435 440 445

Gly Glu Trp Val Asn
450

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids

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- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys	Gly	Glu	Glu	Glu	Thr	Lys	Lys	Thr	Gln	Ala	Ala	Gln	Gln	Pro	Lys	1	5	10	15
Gln	Gln	Thr	Thr	Val	Gln	Gln	Ile	Ala	Val	Gly	Lys	Asp	Ala	Pro	Asp	20	25	30	
Phe	Thr	Leu	Gln	Ser	Met	Asp	Gly	Lys	Glu	Val	Lys	Leu	Ser	Asp	Phe	35	40	45	
Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	Cys	Gly	Pro	50	55	60	
Cys	Lys	Lys	Ser	Met	Pro	Glu	Leu	Met	Glu	Leu	Ala	Ala	Lys	Pro	Asp	65	70	75	80
Arg	Asp	Phe	Glu	Ile	Leu	Thr	Val	Ile	Ala	Pro	Gly	Ile	Gln	Gly	Glu	85	90	95	
Lys	Thr	Val	Glu	Gln	Phe	Pro	Gln	Trp	Phe	Gln	Glu	Gln	Gly	Tyr	Lys	100	105	110	
Asp	Ile	Pro	Val	Leu	Tyr	Asp	Thr	Lys	Ala	Thr	Thr	Ser	Lys	Leu	Ile	115	120	125	
Lys	Phe	Glu	Ala	Phe	Leu	Gln	Asn	Ile	130	135									

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTT	60
TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA	120
TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC	180
tGGAATTGAT GCTGACAATG TCCTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC	240
TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT	300
TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA	360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA	420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGCGG CAGCTGTAGC	480

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CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600
 CATTCGCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960
 CTTCGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTACTACAAA AAGGCTGGTC AAGTCCGTAC 1140
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200
 TGCTCCAAGT GTTGCCATATG ACTTGGAATC TCTCAACCAT GACCCAGTTG CCATGTACTT 1260
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCCTGC 1320
 TGGATTCTCT CAAGGTCTAC CTGTCGGAAT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440
 CGTGATTTTT GGAGGTGACA AC 1462

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr	Phe	Asn	Asn	Lys	Thr	Ile	Glu	Glu	Leu	His	Asn	Leu	Leu	Val	Ser
1				5					10					15	
Lys	Glu	Ile	Ser	Ala	Thr	Glu	Leu	Thr	Gln	Ala	Thr	Leu	Glu	Asn	Ile
			20					25					30		
Lys	Ser	Arg	Glu	Glu	Ala	Leu	Asn	Ser	Phe	Val	Thr	Ile	Ala	Glu	Glu
		35					40					45			
Gln	Ala	Leu	Val	Gln	Ala	Lys	Ala	Ile	Asp	Glu	Ala	Gly	Ile	Asp	Ala
		50				55					60				
Asp	Asn	Val	Leu	Ser	Gly	Ile	Pro	Leu	Ala	Val	Lys	Asp	Asn	Ile	Ser
65					70					75				80	

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Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr
 85 90 95
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly
 100 105 110
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly
 115 120 125
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His
 130 135 140
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala
 145 150 155 160
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile
 165 170 175
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr
 180 185 190
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp
 195 200 205
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu
 210 215 220
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val
 225 230 235 240
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met
 245 250 255
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu
 260 265 270
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly
 275 280 285
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala
 290 295 300
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg
 305 310 315 320
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu
 325 330 335
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val
 340 345 350
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr
 355 360 365
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln
 370 375 380
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr
 385 390 395 400
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val
 405 410 415

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Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn
 485

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACACTAC AAGTCGGCGA CAAGGCGCTT GATTTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTC 300

TTTCGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTCGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser
 1 5 10 15

Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

35	40	45
Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn		
50	55	60
Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg		
65	70	75 80
Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr		
	85	90 95
Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp		
	100	105 110
His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile		
	115	120 125
Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu		
	130	135 140

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA	60
ACAAGACGTT CCCAATTTTG GTTACAANGA TCCAAGACC GGTACTTATT CTGGTATCGA	120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT	180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC	240
CTTTACCATC ACGGACGAAC GCAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA	300
CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG	360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA	420
AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTGGTTCC TACCCAGAAT TGATTACTTC	480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC	540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC	600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA	660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC	720
AGAT	724

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val
1 5 10 15
Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys
20 25 30
Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala
35 40 45
Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr
50 55 60
Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr
65 70 75 80
Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro
85 90 95
Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile
100 105 110
Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly
115 120 125
Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu
130 135 140
Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser
145 150 155 160
Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu
165 170 175
Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys
180 185 190
Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn
195 200 205
Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu
210 215 220
Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala
225 230 235 240
Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTC TTgACTTTCA CTATCTCTCA 60
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAAT TTGGTGAAGA 180
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240
 AGAAGCTGGT CTTGAAGTGG TTGCCCCAACC AAAAATTGAC GTAACCTCAA TGGAAAAAGG 300
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCTGAAGA 420
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480
 AACGCGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCTATC GACGGTGTTG AATTTGACGG 540
 TGGAAAAGGT GAAAACTTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600
 AGACCAATTG GTAGGTCACT CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAGACA TTGATGAAGA 780
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960
 CCTTGGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCAACAAG TTCAAACTT 1200
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260
 AAGCACAGCA ACAGTAAAA 1279

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

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1	5	10	15
Thr Ile Ser Gln Asp Gln Ile Lys Pro Glu Leu Asp Arg Val Phe Lys	20	25	30
Ser Val Lys Lys Ser Leu Asn Val Pro Gly Phe Arg Lys Gly His Leu	35	40	45
Pro Arg Pro Ile Phe Asp Gln Lys Phe Gly Glu Glu Ala Leu Tyr Gln	50	55	60
Asp Ala Met Asn Ala Leu Leu Pro Asn Ala Tyr Glu Ala Ala Val Lys	65	70	75
Glu Ala Gly Leu Glu Val Val Ala Gln Pro Lys Ile Asp Val Thr Ser	85	90	95
Met Glu Lys Gly Gln Asp Trp Val Ile Thr Ala Glu Val Val Thr Lys	100	105	110
Pro Glu Val Lys Leu Gly Asp Tyr Lys Asn Leu Glu Val Ser Val Asp	115	120	125
Val Glu Lys Glu Val Thr Asp Ala Asp Val Glu Glu Arg Ile Glu Arg	130	135	140
Glu Arg Asn Asn Leu Ala Glu Leu Val Ile Lys Glu Ala Ala Ala Glu	145	150	155
Asn Gly Asp Thr Val Val Ile Asp Phe Val Gly Ser Ile Asp Gly Val	165	170	175
Glu Phe Asp Gly Gly Lys Gly Glu Asn Phe Ser Leu Gly Leu Gly Ser	180	185	190
Gly Gln Phe Ile Pro Gly Phe Glu Asp Gln Leu Val Gly His Ser Ala	195	200	205
Gly Glu Thr Val Asp Val Ile Val Thr Phe Pro Glu Asp Tyr Gln Ala	210	215	220
Glu Asp Leu Ala Gly Lys Glu Ala Lys Phe Val Thr Thr Ile His Glu	225	230	235
Val Lys Ala Lys Glu Val Pro Ala Leu Asp Asp Glu Leu Ala Lys Asp	245	250	255
Ile Asp Glu Glu Val Glu Thr Leu Ala Asp Leu Lys Glu Lys Tyr Ser	260	265	270
Lys Glu Leu Ala Ala Ala Lys Glu Glu Ala Tyr Lys Asp Ala Val Glu	275	280	285
Gly Ala Ala Ile Asp Thr Ala Val Glu Asn Ala Glu Ile Val Glu Leu	290	295	300
Pro Glu Glu Met Ile His Glu Glu Val His Arg Ser Val Asn Glu Phe	305	310	315
Leu Gly Asn Leu Gln Arg Gln Gly Ile Asn Pro Asp Met Tyr Phe Gln	325	330	335
Ile Thr Gly Thr Thr Gln Glu Asp Leu His Asn Gln Tyr Gln Ala Glu			

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350

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys
420 425

TGGTCAAAAAG	GAAAGTCAGA	CAGGAAAGGG	GATGAAAATT	GTGACCAGTT	TTTATCCTAT	60
CTACGCTATG	GTTAAGGAAG	TATCTGGTGA	CTTGAATGAT	GTTCGGATGA	TTCAGTCAAG	120
TAGTGGTATT	CACTCCTTTG	AACCTTCGGC	AAATGATATC	GCAGCCATCT	ATGATGCAGA	180
TGTCTTTGTT	TACCATTCTC	ATACACTCGA	ATCTTGGGCA	GGAAGTCTGG	ATCCAAATCT	240
AAAAAAATCC	AAAGTGAAGG	TCTTAGAGGC	TTCTGAGGGA	ATGACCTTGG	AACGTGTCCC	300
TGGACTAGAG	GATGTGGAAG	CAGGGGATGG	AGTTGATGAA	AAAACGCTCT	ATGACCCCTCA	360
CACATGGCTA	GATCCTGAAA	AAGCTGGAGA	AGAAGCCCCA	ATTATCGCTG	ATAAACTTTC	420
AGAGGTGGAT	AGTGAGCATA	AAGAGACTTA	TCAAAAAAAT	GCGCAACCTT	TATCAAAAAA	480
GCTCAGGAAT						490

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 5 10 15

[illegible]

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn
 20 25 30
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro
 35 40 45
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr
 50 55 60
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu
 65 70 75 80
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu
 85 90 95
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp
 100 105 110
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala
 115 120 125
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser
 130 135 140
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys
 145 150 155 160
 Leu Arg Asn

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT 60
 GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG 120
 TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG 180
 TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT 240
 TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT 300
 TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC 360
 AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA 420
 CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA 480
 TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC 540
 AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC 600
 CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA 660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780
 TCCTGTATAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser
 1 5 10 15
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala
 20 25 30
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val
 35 40 45
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala
 50 55 60
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val
 65 70 75 80
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala
 85 90 95
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn
 100 105 110
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu
 115 120 125
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val
 130 135 140
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp
 145 150 155 160
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu
 165 170 175
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln
 180 185 190
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

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195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn 210 215 220		
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser 225 230 235 240		
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala 245 250 255		
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala 260 265 270		
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val 275 280 285		
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met 290 295 300		
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly 305 310 315 320		
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu 325 330 335		

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTAACCTAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAACCTC CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840
TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAAACTAAAG TTCTTGACGT 900
TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTGTC 960
ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala
1 5 10 15
Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn
20 25 30
Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr
35 40 45
Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe
50 55 60
Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu
65 70 75 80
Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr
85 90 95
Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly
100 105 110
Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr
115 120 125
Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val
130 135 140
Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys
145 150 155 160
Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile
165 170 175
His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly
180 185 190
Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn
195 200 205
Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn
210 215 220

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T022T0 2229260

(2) INFORMATION FOR SEQ ID NO: 55:

(A) LENGTH: 2389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCTTACGAG	TTGGGACTGT	ATCAAGCTAG	AACGGTTAAG	GAAAAATAATC	GTGTTTCCTA	60
TATAGATGGA	AAACAAGCGA	CGCAAAAAAC	GGAGAATTTG	ACTCCTGATG	AGGTTAGCAA	120
GCGTGAAGGA	ATCAATGCTG	AGCAAATCGT	CATCAAGATA	ACAGACCAAG	GCTATGTCAC	180
TTCACATGGC	GACCACTATC	ATTATTACAA	TGGTAAGGTT	CCTTATGACG	CTATCATCAG	240
TGAAGAATTA	CTCATGAAAG	ATCCAAACTA	TAAGCTAAAA	GATGAGGATA	TTGTTAATGA	300
GGTCAAGGGT	GGATATGTTA	TCAAGGTAGA	TGGAAAATAC	TATGTTTACC	TTAAGGATGC	360
TGCCCACGCG	GATAACGTCC	GTACAAAAGA	GGAAATCAAT	CGACAAAAAC	AAGAGCATAG	420
TCAACATCGT	GAAGGTGGAA	CTCCAAGAAA	CGATGGTGCT	GTTGCCTTGG	CACGTTTCGA	480
AGGACGCTAT	ACTACAGATG	ATGGTTATAT	CTTTAATGCT	TCTGATATCA	TAGAGGATAC	540
TGGTGATGCT	TATATCGTTC	CTCATGGAGA	TCATTACCAT	TACATTCCTA	AGAATGAGTT	600
ATCAGCTAGC	GAGTTGGCTG	CTGCAGAAGC	CTTCCTATCT	GGTCGAGGAA	ATCTGTCAAA	660
TTCAAGAACC	TATCGCCGAC	AAAATAGCGA	TAACACTTCA	AGAACAAACT	GGGTACCTTC	720
TGTAAGCAAT	CCAGGAACTA	CAAATACTAA	CACAAGCAAC	AACAGCAACA	CTAACAGTCA	780
AGCAAGTCAA	AGTAATGACA	TTGATAGTCT	CTTGAAACAG	CTCTACAAAC	TGCCTTTGAG	840
TCAACGACAT	GTAGAATCTG	ATGGCCTTGT	CTTTGATCCA	GCACAAATCA	CAAGTCGAAC	900
AGCTAGAGGT	GTTGCAGTGC	CACACGGAGA	TCATTACCAC	TTCATCCCTT	ACTCTCAAAAT	960

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020
GGTACCAGAT TCAAGGCCAG AACACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080
CCCGCAACCT GCACCAAATC TTAAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140
ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200
GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAGAGAG 1260
TGTTTCACAC ACTTTAACTG CTAAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320
TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAAGCC TTGTTTGNA AATAAGGGTCG 1380
TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440
TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCCTAGCA CCAATTACCC ATCCAGAGCG 1500
ACTTGGCAAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560
AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTGTGAT GAACATGATA TAATCAGTGA 1620
TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680
CCTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740
TCCATCTCCA GACGCAGATG TTAAAGCAAA TCCAAGTGA GATAGTGCAG CAGCTATTTA 1800
CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860
TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920
TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGAAGA 1980
TTTGTGTCG ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040
TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100
TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160
TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220
AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280
TTTGAATCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340
GTTGTTAAAA GGAAGTAATC CTTATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

1	5	10	15
Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn	20	25	30
Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln	35	40	45
Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp	50	55	60
His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser	65	70	75
Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp	85	90	95
Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys	100	105	110
Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr	115	120	125
Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu	130	135	140
Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln	145	150	155
Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile	165	170	175
Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr	180	185	190
His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala	195	200	205
Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr	210	215	220
Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser	225	230	235
Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn	245	250	255
Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys	260	265	270
Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly	275	280	285
Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val	290	295	300
Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met	305	310	315
Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg	325	330	335
Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln			

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340						345						350					
Pro	Thr	Pro	Glu	Pro	Ser	Pro	Gly	Pro	Gln	Pro	Ala	Pro	Asn	Leu	Lys		
		355					360					365					
Ile	Asp	Ser	Asn	Ser	Ser	Leu	Val	Ser	Gln	Leu	Val	Arg	Lys	Val	Gly		
	370					375					380						
Glu	Gly	Tyr	Val	Phe	Glu	Glu	Lys	Gly	Ile	Ser	Arg	Tyr	Val	Phe	Ala		
385					390					395					400		
Lys	Asp	Leu	Pro	Ser	Glu	Thr	Val	Lys	Asn	Leu	Glu	Ser	Lys	Leu	Ser		
				405					410					415			
Lys	Gln	Glu	Ser	Val	Ser	His	Thr	Leu	Thr	Ala	Lys	Lys	Glu	Asn	Val		
			420					425					430				
Ala	Pro	Arg	Asp	Gln	Glu	Phe	Tyr	Asp	Lys	Ala	Tyr	Asn	Leu	Leu	Thr		
		435				440						445					
Glu	Ala	His	Lys	Ala	Leu	Phe	Xaa	Asn	Lys	Gly	Arg	Asn	Ser	Asp	Phe		
	450					455					460						
Gln	Ala	Leu	Asp	Lys	Leu	Leu	Glu	Arg	Leu	Asn	Asp	Glu	Ser	Thr	Asn		
465					470					475					480		
Lys	Glu	Lys	Leu	Val	Asp	Asp	Leu	Leu	Ala	Phe	Leu	Ala	Pro	Ile	Thr		
				485					490					495			
His	Pro	Glu	Arg	Leu	Gly	Lys	Pro	Asn	Ser	Gln	Ile	Glu	Tyr	Thr	Glu		
			500					505					510				
Asp	Glu	Val	Arg	Ile	Ala	Gln	Leu	Ala	Asp	Lys	Tyr	Thr	Thr	Ser	Asp		
		515					520					525					
Gly	Tyr	Ile	Phe	Asp	Glu	His	Asp	Ile	Ile	Ser	Asp	Glu	Gly	Asp	Ala		
	530					535					540						
Tyr	Val	Thr	Pro	His	Met	Gly	His	Ser	His	Trp	Ile	Gly	Lys	Asp	Ser		
545					550					555					560		
Leu	Ser	Asp	Lys	Glu	Lys	Val	Ala	Ala	Gln	Ala	Tyr	Thr	Lys	Glu	Lys		
				565					570					575			
Gly	Ile	Leu	Pro	Pro	Ser	Pro	Asp	Ala	Asp	Val	Lys	Ala	Asn	Pro	Thr		
			580					585					590				
Gly	Asp	Ser	Ala	Ala	Ala	Ile	Tyr	Asn	Arg	Val	Lys	Gly	Glu	Lys	Arg		
		595				600						605					
Ile	Pro	Leu	Val	Arg	Leu	Pro	Tyr	Met	Val	Glu	His	Thr	Val	Glu	Val		
	610					615					620						
Lys	Asn	Gly	Asn	Leu	Ile	Ile	Pro	His	Lys	Asp	His	Tyr	His	Asn	Ile		
625					630					635					640		
Lys	Phe	Ala	Trp	Phe	Asp	Asp	His	Thr	Tyr	Lys	Ala	Pro	Asn	Gly	Tyr		
				645					650					655			
Thr	Leu	Glu	Asp	Leu	Phe	Ala	Thr	Ile	Lys	Tyr	Tyr	Val	Glu	His	Pro		
			660					665					670				
Asp	Glu	Arg	Pro	His	Ser	Asn	Asp	Gly	Trp	Gly	Asn	Ala	Ser	Glu			

(2) INFORMATION FOR SEQ ID NO: 57:

(A) LENGTH: 1180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TACTGAGATG	CATCATAATC	TAGGAGCTGA	AAAGCGTTCA	GCAGTGGCTA	CTACTATCGA	60
TAGTTTTTAAG	GAGCGAAGTC	AAAAAGTCAG	AGCACTATCT	GATCCAAATG	TGCGTTTTGT	120
TCCCTTCTTT	GGCTCTAGTG	AATGGCTTCG	TTTTGACGGT	GCTCATTC TG	CGGTATTAGC	180
TGAGAAATAC	AATCGTTCCT	ACCGTCCTTA	TCTTTTAGGA	CAGGGGGGAG	CTGCATCGCT	240
TAACCAATAT	TTTGGAATGC	AACAGATGTT	ACCACAGCTG	GAGAATAAAC	AAGTTGTGTA	300
TGTTATCTCA	CCTCAGTGGT	TCAGTAAAAA	TGGCTATGAT	CCAGCAGCCT	TCCAGCAGTA	360
TTTTAATGGA	GACCAGTTGA	CTAGT'TTTTCT	GAAACATCAA	TCTGGGGATC	AGGCTAGTCA	420
ATATGCAGCG	ACTCGCTTAC	TGCAACAGTT	CCCAAACGTA	GCTATGAAGG	ACCTGGTTCA	480
GAAGTTGGCA	AGTAAAGAAG	AATTGTCGAC	AGCAGACAAT	GAAATGATTG	AATTATTGGC	540
TCGTTTTAAT	GAACGCCAAG	CTTCCTTTTT	TGGTCAGTTT	TCGTTTAGAG	GCTATGTTAA	600
CTACGATAAG	CATGTAGCTA	AGTATTTAAA	AATCTTGCCA	GACCAGTTTT	CTTATCAGGC	660
AATAGAAGAT	GTTGTCAAAG	CAGATGCTGA	AAAAAATACT	TCCAATAATG	AGATGGGAAT	720
GGAAAATTAT	TTCTATAATG	AGCAGATCAA	GAAGGATTTG	AAGAAATTAA	AGGATTCTCA	780
GAAAAGCTTT	ACCTATCTCA	AGTCGCCAGA	GTATAATGNN	TTGCAGTTGG	TTTTAACACA	840

(2) INFORMATION FOR SEQ ID NO:58:

(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr 1	Glu	Met	His 5	His	Asn	Leu	Gly	Ala	Glu 10	Lys	Arg	Ser	Ala	Val 15	Ala
Thr	Thr	Ile	Asp 20	Ser	Phe	Lys	Glu	Arg 25	Ser	Gln	Lys	Val	Arg 30	Ala	Leu
Ser	Asp	Pro 35	Asn	Val	Arg	Phe	Val 40	Pro	Phe	Phe	Gly	Ser 45	Ser	Glu	Trp
Leu	Arg 50	Phe	Asp	Gly	Ala	His 55	Ser	Ala	Val	Leu	Ala 60	Glu	Lys	Tyr	Asn
Arg 65	Ser	Tyr	Arg	Pro	Tyr 70	Leu	Leu	Gly	Gln	Gly 75	Gly	Ala	Ala	Ser	Leu 80
Asn	Gln	Tyr	Phe	Gly 85	Met	Gln	Gln	Met	Leu 90	Pro	Gln	Leu	Glu	Asn 95	Lys
Gln	Val	Val	Tyr 100	Val	Ile	Ser	Pro	Gln 105	Trp	Phe	Ser	Lys	Asn 110	Gly	Tyr
Asp	Pro	Ala 115	Ala	Phe	Gln	Gln	Tyr 120	Phe	Asn	Gly	Asp	Gln 125	Leu	Thr	Ser
Phe 130	Leu	Lys	His	Gln	Ser	Gly 135	Asp	Gln	Ala	Ser	Gln 140	Tyr	Ala	Ala	Thr
Arg 145	Leu	Leu	Gln	Gln	Phe 150	Pro	Asn	Val	Ala	Met 155	Lys	Asp	Leu	Val	Gln 160
Lys	Leu	Ala	Ser	Lys 165	Glu	Glu	Leu	Ser	Thr 170	Ala	Asp	Asn	Glu	Met 175	Ile
Glu	Leu	Leu	Ala 180	Arg	Phe	Asn	Glu	Arg 185	Gln	Ala	Ser	Phe	Phe 190	Gly	Gln
Phe	Ser	Val 195	Arg	Gly	Tyr	Val	Asn 200	Tyr	Asp	Lys	His 205	Val	Ala	Lys	Tyr

Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val
 210 215 220
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met
 225 230 235 240
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu
 245 250 255
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn
 260 265 270
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro
 275 280 285
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly
 290 295 300
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln
 305 310 315 320
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly
 325 330 335
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly
 340 345 350
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr
 355 360 365
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp
 370 375 380
 Ala Thr Tyr Asp Gly Asp Val Lys Glu
 385 390

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTATCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420

AAAACTTTCC GCTTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGA CTGAGAC 480
 TTCCTTCAGT CCACTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600
 TGAAGTGATT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660
 GGAAAAAGAG TTA CTGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAT GAGGAATTGA CCTTTAAAT 1140
 GGCCCCAAG GAGGAACTTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCCTCCG 1380
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln
 1 5 10 15
 Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu
 20 25 30
 Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys
 35 40 45
 His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu
 50 55 60
 Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu
 65 70 75 80
 Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

85

90

95

Phe Thr Ile Lys Asp Glu Lys Leu Phe Glu Ile Leu Gln Thr Gln Glu
 100 105 110
 Leu Thr Ala Lys Asn Leu Gln Ser Leu Phe Gln Gly Leu Gly Arg Asp
 115 120 125
 Thr Ala Asn Glu Leu Glu Arg Ile Leu Val Ser Glu Lys Leu Ser Ala
 130 135 140
 Phe Arg Asn Phe Phe Asn Gln Glu Thr Lys Pro Cys Leu Thr Glu Thr
 145 150 155 160
 Ser Phe Ser Pro Val Pro Phe Ala Asn Gln Val Gly Glu Pro Phe Ala
 165 170 175
 Asn Leu Ser Asp Leu Leu Asp Thr Tyr Tyr Lys Asp Lys Ala Glu Arg
 180 185 190
 Asp Arg Val Lys Gln Gln Ala Ser Glu Leu Ile Arg Arg Val Glu Asn
 195 200 205
 Glu Leu Gln Lys Asn Arg His Lys Leu Lys Lys Gln Glu Lys Glu Leu
 210 215 220
 Leu Ala Thr Asp Asn Ala Glu Glu Phe Arg Gln Lys Gly Glu Leu Leu
 225 230 235 240
 Thr Thr Phe Leu His Gln Val Pro Asn Asp Gln Asp Gln Val Ile Leu
 245 250 255
 Asp Asn Tyr Tyr Thr Asn Gln Pro Ile Met Ile Ala Leu Asp Lys Ala
 260 265 270
 Leu Thr Pro Asn Gln Asn Ala Gln Arg Tyr Phe Lys Arg Tyr Gln Lys
 275 280 285
 Leu Lys Glu Ala Val Lys Tyr Leu Thr Asp Leu Ile Glu Glu Thr Lys
 290 295 300
 Ala Thr Ile Leu Tyr Leu Glu Ser Val Glu Thr Val Leu Asn Gln Ala
 305 310 315 320
 Gly Leu Glu Glu Ile Ala Glu Ile Arg Glu Glu Leu Ile Gln Thr Gly
 325 330 335
 Phe Ile Arg Arg Arg Gln Arg Glu Lys Ile Gln Lys Arg Lys Lys Leu
 340 345 350
 Glu Gln Tyr Leu Ala Ser Asp Gly Lys Thr Ile Ile Tyr Val Gly Arg
 355 360 365
 Asn Asn Leu Gln Asn Glu Glu Leu Thr Phe Lys Met Ala Arg Lys Glu
 370 375 380
 Glu Leu Trp Phe His Ala Lys Asp Ile Pro Gly Ser His Val Val Ile
 385 390 395 400
 Ser Gly Asn Leu Asp Pro Ser Asp Ala Val Lys Thr Asp Ala Ala Glu
 405 410 415
 Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val

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173

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro
435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp
450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser
465 470

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA	60
AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC	120
CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC	180
ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG	240
TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA	300
AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT	360
TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT	420
AGAAGCTGGC TACACTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT	480
CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA	540
TGCC	544

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys	
1 5 10 15	

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn	
20 25 30	

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln	
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35	40	45
Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg		
50	55	60
Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys		
65	70	75 80
Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp		
	85	90 95
Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro		
	100	105 110
Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys		
	115	120 125
Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr		
	130	135 140
Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile		
	145	150 155 160
Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu		
	165	170 175
Leu Gln Pro Tyr Ala		
	180	

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGGTGGTT TGAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT	240
GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGA	360
ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA	420
GACTGATTTT GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTAGC 720
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780
 AGAGAGGGCG CATAGTCAAT TTAAAAATGA A 811

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala	Lys	Glu	Arg	Val	Asp	Val	Leu	Ala	Tyr	Lys	Gln	Gly	Leu	Phe	Glu	1	5	10	15							
Thr	Arg	Glu	Gln	Ala	Lys	Arg	Gly	Val	Met	Ala	Gly	Leu	Val	Val	Ala	20	25	30								
Val	Leu	Asn	Gly	Glu	Arg	Phe	Asp	Lys	Pro	Gly	Glu	Lys	Ile	Pro	Asp	35	40	45								
Asp	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Glu	Lys	Leu	Lys	Tyr	Val	Ser	Arg	50	55	60								
Gly	Gly	Leu	Lys	Leu	Glu	Lys	Ala	Leu	Gln	Val	Phe	Asp	Leu	Ser	Val	65	70	75								
Asp	Gly	Ala	Thr	Thr	Ile	Asp	Ile	Gly	Ala	Ser	Thr	Gly	Gly	Phe	Thr	85	90	95								
Asp	Val	Met	Leu	Gln	Asn	Ser	Ala	Lys	Leu	Val	Phe	Ala	Val	Asp	Val	100	105	110								
Gly	Thr	Asn	Gln	Leu	Ala	Trp	Lys	Leu	Arg	Gln	Asp	Pro	Arg	Val	Val	115	120	125								
Ser	Met	Glu	Gln	Phe	Asn	Phe	Arg	Tyr	Ala	Glu	Lys	Thr	Asp	Phe	Glu	130	135	140								
Gln	Glu	Pro	Ser	Phe	Ala	Ser	Ile	Asp	Val	Ser	Phe	Ile	Ser	Leu	Ser	145	150	155								
Leu	Ile	Leu	Pro	Ala	Leu	His	Arg	Val	Leu	Ala	Asp	Gln	Gly	Gln	Val	165	170	175								
Val	Ala	Leu	Val	Lys	Pro	Gln	Phe	Glu	Ala	Gly	Arg	Glu	Gln	Ile	Gly	180	185	190								
Lys	Asn	Gly	Ile	Ile	Arg	Asp	Ala	Lys	Val	His	Gln	Asn	Val	Leu	Glu	195	200	205								
Ser	Val	Thr	Ala	Met	Ala	Val	Glu	Val	Gly	Phe	Ser	Val	Leu	Gly	Leu	210	215	220								
Asp	Phe	Ser	Pro	Ile	Gln	Gly	Gly	His	Gly	Asn	Ile	Glu	Phe	Leu	Ala	225	230	235								

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Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTAT GAACCTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCCCTT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAAACGGT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCTTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GA CTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAACGA ATTGCTCGTA TTATTCCCCT	960
TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GA CTCCGGA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTCGAAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC	1200
AGGCATTGAT AGCAAACCTGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

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AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620
 TATGACCCAT AGCCACTGGA TTAAAAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTCAGG 1740
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160
 ACCAGAGTCT CCAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280
 AATCCAGGAT 2290

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

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Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala Glu
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser Ser
 210 215 220
 Tyr Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr
 290 295 300
 Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn

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420	425	430
Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn 435 440 445		
Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg 450 455 460		
Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu 465 470 475 480		
Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn 485 490 495		
Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala 500 505 510		
Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile 515 520 525		
Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser 530 535 540		
His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala 545 550 555 560		
Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His 565 570 575		
Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn 580 585 590		
Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn 595 600 605		
Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His 610 615 620		
Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu 625 630 635 640		
Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val 645 650 655		
Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly 660 665 670		
Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala 675 680 685		
Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu 690 695 700		
Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys 705 710 715 720		
Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu 725 730 735		
Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg 740 745 750		
Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp		

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755

760

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA      60
AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAAACCTGT      120
ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA      180
AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA      240
TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT      300
TCTTGATAAA AACAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG              352

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(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile
1           5           10           15
Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser
          20           25           30
Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys
          35           40           45
Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn
          50           55           60
Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp
          65           70           75           80
Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val
          85           90           95
Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr
          100          105          110
Asn Asn Pro Asn Lys
          115

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(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG	60
TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA	120
AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC	180
GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA	240
AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA	300
ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT	360
TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC	420
TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT	480
TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT	540
AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA	600
GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC	660
TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA	720
TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT	780
ACCTTGGAAT AATGGTGTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA	840
GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG	900
TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA	960
GAGTGCATAT GGGAACTGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCGG	1020
TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA	1080
TCAATGGAAT AAATGGAACA ATCATTGGTT CTATTGACA GACTCTGGTG CTTCTGCTAA	1140
AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT	1200
TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC	1260
AGGATGGCTT CAATATATGG GGCAATGGTA TACTTTGCT CCATCAGGGG AA	1312

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

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Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys Ile His Phe Ile Asn
1           5           10           15
Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu Glu Ser Asn Gly His
20           25           30
Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp Phe Pro Asp Gly Ser
35           40           45
Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu Thr Ser Tyr Lys His
50           55           60
Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys Glu Leu Gly Val Gln
65           70           75           80
Lys Leu Asp Phe Ile Leu Val Thr His Thr His Ser Asp His Ile Gly
85           90           95
Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val Asp Arg Val Tyr Leu
100          105          110
Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser Glu Arg Leu Trp Asp
115          120          125
Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr Ala Ala Glu Lys Gly
130          135          140
Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp Ala His Phe Gln Phe
145          150          155          160
Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu Asn Glu Thr Asp Ser
165          170          175
Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn Ser Asn Ser Leu Ile
180          185          190
Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr Leu Gly Gly Asp Leu
195          200          205
Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly Pro Leu Ile Gly Lys
210          215          220
Val Asp Leu Met Lys Phe Asn His His His Asp Thr Asn Lys Ser Asn
225          230          235          240
Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser Leu Ile Val Gln Thr
245          250          255
Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp Ser Glu Tyr Val Asn
260          265          270
Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn Ala Ala Ser Lys Asp
275          280          285
Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp Gly Phe Val Asn Ile
290          295          300

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Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys
 305 310 315 320

Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu
 325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn
 340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His
 355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys
 370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile
 385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly
 405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe
 420 425 430

Ala Pro Ser Gly Glu
 435

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGCGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCCTCTTT GACATCATTG CCCAGTCTAT 840
 CAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960
 ACGTACTAAA CAATTCCGTG ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAATG GAACTAGCCA 1560
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTT GAAACGAATC 1800
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe
 1 5 10 15
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser
 20 25 30
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu
 35 40 45
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala
 50 55 60

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Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala
 65 70 75 80
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu
 85 90 95
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro
 100 105 110
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr
 115 120 125
 Lys Arg Leu Leu Ile Asp Ser Ile Lys Tyr Leu Val Asp Thr Tyr Lys
 130 135 140
 Val Asp Gly Phe Arg Phe Asp Met Met Gly Asp His Asp Ala Ala Ser
 145 150 155 160
 Ile Glu Glu Ala Tyr Lys Ala Ala Arg Ala Leu Asn Pro Asn Leu Ile
 165 170 175
 Met Leu Gly Glu Gly Trp Arg Thr Tyr Ala Gly Asp Glu Asn Met Pro
 180 185 190
 Thr Lys Ala Ala Asp Gln Asp Trp Met Lys His Thr Asp Thr Val Ala
 195 200 205
 Val Phe Ser Asp Asp Ile Arg Asn Asn Leu Lys Ser Gly Tyr Pro Asn
 210 215 220
 Glu Gly Gln Pro Ala Phe Ile Thr Gly Gly Lys Arg Asp Val Asn Thr
 225 230 235 240
 Ile Phe Lys Asn Leu Ile Ala Gln Pro Thr Asn Phe Glu Ala Asp Ser
 245 250 255
 Pro Gly Asp Val Ile Gln Tyr Ile Ala Ala His Asp Asn Leu Thr Leu
 260 265 270
 Phe Asp Ile Ile Ala Gln Ser Ile Lys Lys Asp Pro Ser Lys Ala Glu
 275 280 285
 Asn Tyr Ala Glu Ile His Arg Arg Leu Arg Leu Gly Asn Leu Met Val
 290 295 300
 Leu Thr Ala Gln Gly Thr Pro Phe Ile His Ser Gly Gln Glu Tyr Gly
 305 310 315 320
 Arg Thr Lys Gln Phe Arg Asp Pro Ala Tyr Lys Thr Pro Val Ala Glu
 325 330 335
 Asp Lys Val Pro Asn Lys Ser His Leu Leu Arg Asp Lys Asp Gly Asn
 340 345 350
 Pro Phe Asp Tyr Pro Tyr Phe Ile His Asp Ser Tyr Asp Ser Ser Asp
 355 360 365
 Ala Val Asn Lys Phe Asp Trp Thr Lys Ala Thr Asp Gly Lys Ala Tyr
 370 375 380
 Pro Glu Asn Val Lys Ser Arg Asp Tyr Met Lys Gly Leu Ile Ala Leu
 385 390 395 400

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Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys
405 410 415

Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys
420 425 430

Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile
435 440 445

Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu
450 455 460

Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu
465 470 475 480

Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp
485 490 495

Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg
500 505 510

Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro
515 520 525

Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro
530 535 540

Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro
545 550 555 560

Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala
565 570 575

Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val
580 585 590

Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn
595 600 605

Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu
610 615

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGCAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480
 AGTACAGCAA GGTGGCTTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTGGTA 720
 CTA CTCTCAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780
 GTTTTACCTC AAATCTGATG GGAAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320
 TTTCAAAGAT TTAACAGAGG CTACAAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380
 TTTGCTAAAC ATTAACAATA GCCTTTTGGG GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500
 GGGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGGAAGAACT TTCCTTGGA ACAAGGCTTC 1680
 TGGTATGAAT GTGGAATATG CTTGAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

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Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser
 1 5 10 15
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe
 20 25 30
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln
 35 40 45
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser
 50 55 60
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly
 65 70 75 80
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr
 85 90 95
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala
 100 105 110
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu
 115 120 125
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu
 130 135 140
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys
 145 150 155 160
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr
 165 170 175
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn
 180 185 190
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu
 195 200 205
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys
 210 215 220
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr
 225 230 235 240
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp
 245 250 255
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys
 260 265 270
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser
 275 280 285
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly
 290 295 300
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala
 305 310 315 320
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly
 325 330 335

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Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys
 340 345 350
 Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu
 355 360 365
 Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys
 370 375 380
 Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr
 385 390 395 400
 Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met
 405 410 415
 Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly
 420 425 430
 Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr
 435 440 445
 Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile
 450 455 460
 Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu
 465 470 475 480
 Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu
 485 490 495
 Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe
 500 505 510
 Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr
 515 520 525
 Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys
 530 535 540
 Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser
 545 550 555 560
 Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile
 565 570 575
 Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp
 580 585 590

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:-----

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC 180
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT 300
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTAATAAATA 360
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420
GAAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG 480
TACTTTAAGT CAAAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540
AGTTCTTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660
GGTAGATGAA CGTGATGGAA CAATTGAAGA AACTACTTCT CGTCAAATTA CTAAAGAGAT 720
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080
CAATGATAAT GGTGAATGGG TCGCT 1105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile
1 5 10 15
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr
20 25 30
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr
35 40 45
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp
50 55 60
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro
65 70 75 80

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(2) INFORMATION FOR SEQ ID NO: 77:

(A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTTATC TCCAACATTA 60
TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120
ACCTAATGCT CAGGCTGTTT ACTTGTTGGG TGATTTTACC AACTGGATTG AAAATCAGAT 180
TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240
GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300
TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360
GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420
TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480
TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAATATAC 540
TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600
TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660
C 661

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr
1 5 10 15
Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His
20 25 30
Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu
35 40 45
Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg
50 55 60
Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly
65 70 75 80
His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met
85 90 95
Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly
100 105 110
Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
165	170	175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
180	185	190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
195	200	205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
210	215	220

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 976 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTGTC GAGGAGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGGA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAGCAT TGGATTGATG TCTATCATTT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCT CAGGCTTGCG CAATCTCTAT ACGTACCAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCAATGAAT GCTAAGATGA AGTATTTCCG	840
TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA	900
TGATGGTATT GAAATCATTT ATGCGGATAA TCGAGACCAG AGTGTTCTTT CCTTTATTCG	960

TAAGGGTAAA AAGGGA

976

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

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Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15

Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
          20           25           30

Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
          35           40           45

His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
          50           55           60

Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
65           70           75           80

Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
          85           90           95

Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
          100          105          110

Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
          115          120          125

Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
          130          135          140

Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
          145          150          155          160

Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
          165          170          175

Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
          180          185          190

Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
          195          200          205

His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
          210          215          220

Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
          225          230          235          240

Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
          245          250          255

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Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met
 260 265 270
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys
 275 280 285
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu
 290 295 300
 Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg
 305 310 315 320
 Lys Gly Lys Lys Gly
 325

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA 60
 AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120
 GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA 180
 AGCCGTAACT CCAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT 240
 AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA 300
 TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360
 TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420
 AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC 480
 ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAAC 540
 AGATGAAAAA GACCTCAAGA AAAATGTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC 600
 TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660
 ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720
 AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780
 TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840
 ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900
 GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960
 TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020
 AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC 1080

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CTTGTACGAA TTGATTACGC GTGTTTACCG TGACGGTCAA TTGGTTGATG CTAAGAAGGA 1140
 TTTGTTTGGT TACCGTTACT ATCACTGGAC TCCAAATGAA GGTTCCTCTT TGAATGGTGA 1200
 ACGTATTAAA TTCCATGGAG TATCCTTGCA CCACGACCAT GGGGCGCTTG GAGCAGAAGA 1260
 AAACTATAAA GCAGAATATC GCCGTCTCAA ACAAATGAAG GAGATGGGAG TTAAGTCCAT 1320
 CCGTACAACC CACAACCCTG CTAGTGAGCA AACCTTGCAA ATCGCAGCAG AACTAGGTTT 1380
 ACTCGTTCAG GAAGAGGCCT TTGATACGTG GTATGGTGGC AAGAAACCTT ATGACTATGG 1440
 ACGTTTCTTT GAAAAAGATG CCACTCACCC AGAAGCTCGA AAAGGTGAAA AATGGTCTGA 1500
 TTTTGACCTA CGTACCATGG TCGAAAGAGG CAAAAACAAC CCTGCTATCT TCATGTGGTC 1560
 AATTGGTAAT GAAATAGGTG AAGCTAATGG TGATGCCAC TCTTTAGCAA CTGTTAAACG 1620
 TTTGGTTAAG GTTATCAAGG ATGTTGATAA GACTCGCTAT GTTACCATGG GAGCAGATAA 1680
 ATTCCGTTTC GGTAATGGTA GCGGAGGGCA TGAGAAAATT GCTGATGAAC TCGATGCTGT 1740
 TGGATTTAAC TATTCTGAAG ATAATTACAA AGCCCTTAGA GCTAAGCATC CAAAATGGTT 1800
 GATTTATGGA TCAGAAACAT CTTGAGCTAC CCGTACACGT GGAAGTTACT ATCGCCCTGA 1860
 ACGTGAATTG AAACATAGCA ATGGACCTGA GCGTAATTAT GAACAGTCAG ATTATGGAAA 1920
 TGATCGTGTG GGTGGGGGA AAACAGCAAC CGCTTCATGG ACTTTTGACC GTGACAACGC 1980
 TGGCTATGCT GGACAGTTTA TCTGGACAGG TACGGACTAT ATTGGTGAAC CTACACCATG 2040
 GCACAACCAA AATCAAACCTC CTGTTAAGAG CTCTTACTTT GGTATCGTAG ATACAGCCGG 2100
 CATTCCAAAA CATGACTTCT ATCTCTACCA AAGC 2134

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Val Val Tyr Ala Asp Glu Thr Leu Ile Thr His Thr Ala Glu Lys
 1 5 10 15

Pro Lys Glu Glu Lys Met Ile Val Glu Glu Lys Ala Asp Lys Ala Leu
 20 25 30

Glu Thr Lys Asn Ile Val Glu Arg Thr Glu Gln Ser Glu Pro Ser Ser
 35 40 45

Thr Glu Ala Ile-Ala Ser Glu Xaa Lys Glu Asp Glu Ala Val Thr Pro
 50 55 60

Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

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65	70	75	80
Glu Ser Gln Ala Ser Asn Gln Glu Lys Pro Leu Lys Glu Asp Ala Lys	85	90	95
Ala Val Thr Asn Glu Glu Val Asn Gln Met Ile Glu Asp Arg Lys Val	100	105	110
Asp Phe Asn Gln Asn Trp Tyr Phe Lys Leu Asn Ala Asn Ser Lys Glu	115	120	125
Ala Ile Lys Pro Asp Ala Asp Val Ser Thr Trp Lys Lys Leu Asp Leu	130	135	140
Pro Tyr Asp Trp Ser Ile Phe Asn Asp Phe Asp His Glu Ser Pro Ala	145	150	155
Gln Asn Glu Gly Gly Gln Leu Asn Gly Gly Glu Ala Trp Tyr Arg Lys	165	170	175
Thr Phe Lys Leu Asp Glu Lys Asp Leu Lys Lys Asn Val Arg Leu Thr	180	185	190
Phe Asp Gly Val Tyr Met Asp Ser Gln Val Tyr Val Asn Gly Gln Leu	195	200	205
Val Gly His Tyr Pro Asn Gly Tyr Asn Gln Phe Ser Tyr Asp Ile Thr	210	215	220
Lys Tyr Leu Gln Lys Asp Gly Arg Glu Asn Val Ile Ala Val His Ala	225	230	235
Val Asn Lys Gln Pro Ser Ser Arg Trp Tyr Ser Gly Ser Gly Ile Tyr	245	250	255
Arg Asp Val Thr Leu Gln Val Thr Asp Lys Val His Val Glu Lys Asn	260	265	270
Gly Thr Thr Ile Leu Thr Pro Lys Leu Glu Glu Gln Gln His Gly Lys	275	280	285
Val Glu Thr His Val Thr Ser Lys Ile Val Asn Thr Asp Asp Lys Asp	290	295	300
His Glu Leu Val Ala Glu Tyr Gln Ile Val Glu Arg Gly Gly His Ala	305	310	315
Val Thr Gly Leu Val Arg Thr Ala Ser Arg Thr Leu Lys Ala His Glu	325	330	335
Ser Thr Ser Leu Asp Ala Ile Leu Glu Val Glu Arg Pro Lys Leu Trp	340	345	350
Thr Val Leu Asn Asp Lys Pro Ala Leu Tyr Glu Leu Ile Thr Arg Val	355	360	365
Tyr Arg Asp Gly Gln Leu Val Asp Ala Lys Lys Asp Leu Phe Gly Tyr	370	375	380
Arg Tyr Tyr His Trp Thr Pro Asn Glu Gly Phe Ser Leu Asn Gly Glu	385	390	395
Arg Ile Lys Phe His Gly Val Ser Leu His His Asp His Gly Ala Leu			400

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405 410 415
 Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met
 420 425 430
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser
 435 440 445
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu
 450 455 460
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly
 465 470 475 480
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu
 485 490 495
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn
 500 505 510
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala
 515 520 525
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val
 530 535 540
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys
 545 550 555 560
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu
 565 570 575
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu
 580 585 590
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser
 595 600 605
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys
 610 615 620
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn
 625 630 635 640
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp
 645 650 655
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp
 660 665 670
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val
 675 680 685
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His
 690 695 700
 Asp Phe Tyr Leu Tyr Gln Ser
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTTCG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAAGTGGT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAAATT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860
 CACTTGGCAA GCTATTCCGA AAGAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040
 TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTCCG 2100
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTGCTTAG AAGGTACGCA 2160
 ATTAACA 2167

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr
 1 5 10 15
 Leu Tyr Gln Ser Gln Trp Val Ser Val Lys Lys Lys Pro Met Val His
 20 25 30
 Leu Leu Pro His Trp Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val
 35 40 45
 Ala Asp Ser Glu Gly Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser
 50 55 60
 Ser Val Glu Leu Phe Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe
 65 70 75 80
 Asn Lys Lys Gln Thr Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn
 85 90 95
 Ala Asn Glu Leu Tyr Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr
 100 105 110
 Leu Glu Ala Ile Ala Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp
 115 120 125
 Lys Ile Thr Thr Ala Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu
 130 135 140
 Asp His Ala Ile Ala Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr
 145 150 155 160
 Glu Ile Val Asp Ser Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu

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201

165

170

175

Val Arg Phe Gln Leu His Gly Gln Gly Gln Leu Val Gly Val Asp Asn
 180 185 190
 Gly Glu Gln Ala Ser Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser
 195 200 205
 Trp Ile Arg Lys Ala Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser
 210 215 220
 Thr Glu Gln Ala Gly Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu
 225 230 235 240
 Lys Ser Asn Gln Val Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu
 245 250 255
 Lys Thr Val Leu Gly Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly
 260 265 270
 Glu Ala Pro Glu Met Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly
 275 280 285
 Ser Arg Ala Glu Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys
 290 295 300
 Pro Gly Ile Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu
 305 310 315 320
 Ala Arg Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys
 325 330 335
 Arg Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser
 340 345 350
 Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp
 355 360 365
 Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg
 370 375 380
 Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu
 385 390 395 400
 Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr
 405 410 415
 Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln
 420 425 430
 Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser
 435 440 445
 Ala Lys Asn Ala Ala Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly
 450 455 460
 Met Arg Ala Ser Ile Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln
 465 470 475 480
 Thr Tyr Ala Ile Gln Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu
 485 490 495
 Ser Leu Gln Val Glu Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val

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500	505	510
Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu 515	520	525
Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala 530	535	540
Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu 545	550	555
Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln 565	570	575
Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val 580	585	590
Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val 595	600	605
Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala 610	615	620
Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly 625	630	635
Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu 645	650	655
Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu 660	665	670
Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His 675	680	685
Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr 690	695	700
Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln 705	710	715
Leu Thr		

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT GCGTATCTGC	120
TCAAACCTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTC	240

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CTACAATAAC CAACCAGCCA ATCGTTGGAC AAACCTGGAAT CGTACTAATC CAGAAGCTTC	300
AGTCGGTGTT CTGTTTGGAG ATTCAGGTAT CTTGAGCAAA CGCTCCGTTG ATAATCTAAG	360
TGTCGGATTC CATGAAGACC ATGGAGTTGG TGTACCGAAG TCTTATGTGA TTGAGTATTA	420
TGTTGGTAAG ACTGTCCCAA CAGCTCCTAA AAACCCTAGT TTTGTTGGTA ATGAGGACCA	480
TGTCTTTAAT GATTCTGCCA ACTGGAAACC AGTTACTAAT CTAAAAGCCC CTGCTCAACT	540
CAAGGCTGGA GAAATGAACC ACTTTAGCTT TGATAAAGTT GAAACCTATG CTGTTTCGTAT	600
TCGCATGGTT AAAGCAGATA ACAAGCGTGG AACGTCTATC ACAGAGGTAC AAATCTTTCG	660
GAAACAAGTT GCGGCAGCCA AGCAAGGACA AACAAGAATC CAAGTTGACG GCAAAGACTT	720
AGCAAACCTC AACCCGTGATT TGACAGACTA CTACCTTGAG TCTGTAGATG GAAAAGTTCC	780
GGCAGTCACA GCAAGTGTTA GCAACAATGG TCTCGCTACC GTCGTTCCAA GCGTTCGTGA	840
AGGTGAGCCA GTTCGTGTCA TCGCGAAAGC TGAAAATGGC GACATCTTAG GAGAATACCG	900
TCTGCACTTC ACTAAGGATA AGAGCTTACT TTCTCATAAA CCAGTTGCTG CGGTTAAACA	960
AGCTCGCTTG CTACAAGTAG GTCAAGCACT TGAATTGCCG ACTAAGGTTC CAGTTTACTT	1020
CACAGGTAAA GACGGCTACG AAACAAAAGA CCTGACAGTT GAATGGGAAG AAGTTCCAGC	1080
GGAAAATCTG AAAAAAGCAG GTCAATTTAC TGTTTCGAGGC CGTGTCCCTG GTAGTAACCT	1140
TGTTGCTGAG ATCACTGTAC GAGTGACAGA CAAACTTGGT GAGACTCTTT CAGATAACCC	1200
TAAGTATGAT GAAAACAGTA ACCAGGCCTT TGCTTCAGCA ACCAATGATA TTGACAAAAA	1260
CTCTCATGAC CGCGTTGACT ATCTCAATGA CGGAGATCAT TCAGAAAATC GTCGTTGGAC	1320
AAACTGGTCA CCAACACCAT CTTCTAATCC AGAAGTATCA GCGGGTGTGA TTTTCCGTGA	1380
AAATGGTAAG ATTGTAGAAC GGACTGTTAC ACAAGGAAAA GTTCAGTTCT TTGCAGATAG	1440
TGGTACGGAT GCACCATCTA AACTCGTTTT AGAACGCTAT GTCGGTCCAG AGTTTGAAGT	1500
GCCAACCTAC TATTCAAACCT ACCAAGCCTA CGACGCAGAC CATCCATTCA ACAATCCAGA	1560
AAATTGGGAA GCTGTTCCCTT ATCGTGCGGA TAAAGACATT GCAGCTGGTG ATGAAATCAA	1620
CGTAACATTT AAAGCTATCA AAGCCAAAGC TATGAGATGG CGTATGGAGC GTAAAGCAGA	1680
TAAGAGCGGT GTTGCGATGA TTGAGATGAC CTTCCCTGCA CCAAGTGAAT TGCCTCAAGA	1740
AAGCACTCAA TCAAAGATTC TTGTAGATGG AAAAGAACTT GCTGATTTCG CTGAAAATCG	1800
TCAAGACTAT CAAATTACCT ATAAAGGTCA ACGGCCAAAA GTCTCAGTTG AAGAAAACAA	1860
TCAAGTAGCT TCAACTGTGG TAGATAGTGG AGAAGATAGC TTTCCAGTAC TTGTTTCGCTT	1920
CGTTTCAGAA AGTGGAAAAC AAGTCAAGGA ATACCGTATC CACTTGACTA AGGAAAAACC	1980
AGTTTCTGAG AAGACAGTTG CTGCTGTACA AGAAGATCTT CCAAAAATCG AATTTGTTGA	2040
AAAAGATTTG GCATACAAGA CAGTTGAGAA AAAAGATTCA AACTGTATC TAGGTGAAAC	2100

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TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220
 GGTGGAACC AAACAGTAG CTCAAGAAGC TAAAAACCA CAAGTGTGAG AAAAAGCAGA 2280
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu
 1 5 10 15
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr
 20 25 30
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile
 35 40 45
 Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp
 50 55 60
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser
 65 70 75 80
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn
 85 90 95
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser
 100 105 110
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly
 115 120 125
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr
 130 135 140
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His
 145 150 155 160
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala
 165 170 175
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys
 180 185 190
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys
 195 200 205
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala
 210 215 220

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 102210 225460

Ala	Ala	Lys	Gln	Gly	Gln	Thr	Arg	Ile	Gln	Val	Asp	Gly	Lys	Asp	Leu	225	230	235	240
Ala	Asn	Phe	Asn	Pro	Asp	Leu	Thr	Asp	Tyr	Tyr	Leu	Glu	Ser	Val	Asp	245	250	255	
Gly	Lys	Val	Pro	Ala	Val	Thr	Ala	Ser	Val	Ser	Asn	Asn	Gly	Leu	Ala	260	265	270	
Thr	Val	Val	Pro	Ser	Val	Arg	Glu	Gly	Glu	Pro	Val	Arg	Val	Ile	Ala	275	280	285	
Lys	Ala	Glu	Asn	Gly	Asp	Ile	Leu	Gly	Glu	Tyr	Arg	Leu	His	Phe	Thr	290	295	300	
Lys	Asp	Lys	Ser	Leu	Leu	Ser	His	Lys	Pro	Val	Ala	Ala	Val	Lys	Gln	305	310	315	320
Ala	Arg	Leu	Leu	Gln	Val	Gly	Gln	Ala	Leu	Glu	Leu	Pro	Thr	Lys	Val	325	330	335	
Pro	Val	Tyr	Phe	Thr	Gly	Lys	Asp	Gly	Tyr	Glu	Thr	Lys	Asp	Leu	Thr	340	345	350	
Val	Glu	Trp	Glu	Glu	Val	Pro	Ala	Glu	Asn	Leu	Thr	Lys	Ala	Gly	Gln	355	360	365	
Phe	Thr	Val	Arg	Gly	Arg	Val	Leu	Gly	Ser	Asn	Leu	Val	Ala	Glu	Ile	370	375	380	
Thr	Val	Arg	Val	Thr	Asp	Lys	Leu	Gly	Glu	Thr	Leu	Ser	Asp	Asn	Pro	385	390	395	400
Asn	Tyr	Asp	Glu	Asn	Ser	Asn	Gln	Ala	Phe	Ala	Ser	Ala	Thr	Asn	Asp	405	410	415	
Ile	Asp	Lys	Asn	Ser	His	Asp	Arg	Val	Asp	Tyr	Leu	Asn	Asp	Gly	Asp	420	425	430	
His	Ser	Glu	Asn	Arg	Arg	Trp	Thr	Asn	Trp	Ser	Pro	Thr	Pro	Ser	Ser	435	440	445	
Asn	Pro	Glu	Val	Ser	Ala	Gly	Val	Ile	Phe	Arg	Glu	Asn	Gly	Lys	Ile	450	455	460	
Val	Glu	Arg	Thr	Val	Thr	Gln	Gly	Lys	Val	Gln	Phe	Phe	Ala	Asp	Ser	465	470	475	480
Gly	Thr	Asp	Ala	Pro	Ser	Lys	Leu	Val	Leu	Glu	Arg	Tyr	Val	Gly	Pro	485	490	495	
Glu	Phe	Glu	Val	Pro	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gln	Ala	Tyr	Asp	Ala	500	505	510	
Asp	His	Pro	Phe	Asn	Asn	Pro	Glu	Asn	Trp	Glu	Ala	Val	Pro	Tyr	Arg	515	520	525	
Ala	Asp	Lys	Asp	Ile	Ala	Ala	Gly	Asp	Glu	Ile	Asn	Val	Thr	Phe	Lys	530	535	540	
Ala	Ile	Lys	Ala	Lys	Ala	Met	Arg	Trp	Arg	Met	Glu	Arg	Lys	Ala	Asp	545	550	555	560

Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
565 570 575

Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu
580 585 590

Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys
595 600 605

Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser
610 615 620

Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu
625 630 635 640

Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr
645 650 655

Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp
660 665 670

Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val
675 680 685

Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln
690 695 700

Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp
705 710 715 720

Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp
725 730 735

Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys
740 745 750

Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu
755 760 765

Ala Ser Gln Thr Asn Lys Ala Gln
770 775

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG	60
AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA	120
AACAGGGACA GAA	133

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1           5           10           15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
20           25           30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
35           40

```

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 775 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAAATAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT          775

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala Arg Thr Glu Asn
 1 5 10 15
 Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu Ala Pro Lys Thr
 20 25 30
 Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val Lys Pro Thr Asp
 35 40 45
 Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp Ser Ala Glu Pro
 50 55 60
 Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser Lys Pro Glu Glu
 65 70 75 80
 Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp Lys Pro Ala Glu
 85 90 95
 Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp
 100 105 110
 Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Ala Pro Glu Glu
 115 120 125
 Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu Ser Thr Pro Asp
 130 135 140
 Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu Thr Val Asn Gln
 145 150 155 160
 Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val Glu Lys Gln Thr
 165 170 175
 Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 180 185 190
 Pro Arg Glu Asp Glu Gln Ala Pro Thr Ala Pro Val Glu Pro Glu Lys
 195 200 205
 Gln Pro Glu Val Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys
 210 215 220
 Pro Glu Asp Lys Ile Lys Gly Ile Gly Thr Lys Glu Pro Val Asp Lys
 225 230 235 240
 Ser Glu Leu Asn Asn Gln Ile Asp Lys Ala Ser Ser Val Ser Pro Thr
 245 250 255
 Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TAATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                     199

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15
Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
          20           25           30
Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
          35           40           45
Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
          50           55           60
Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC      120
TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT      180
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT      240

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TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTCGAC 360
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420
 AAAAACTGTA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAT 540
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780
 ACTAGACCTT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Lys	Gly	Glu	Thr	Glu	Val	Gln	Pro	Glu	Ser	Pro	Asp	Thr	Val	Val	1	5	10	15
Ser	Asp	Lys	Gly	Glu	Pro	Glu	Gln	Val	Ala	Pro	Leu	Pro	Glu	Tyr	Lys	20	25	30	
Gly	Asn	Ile	Glu	Gln	Val	Lys	Pro	Glu	Thr	Pro	Val	Glu	Lys	Thr	Lys	35	40	45	
Glu	Gln	Gly	Pro	Glu	Lys	Thr	Glu	Glu	Val	Pro	Val	Lys	Pro	Thr	Glu	50	55	60	
Glu	Thr	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Thr	Glu	Gly	Thr	Ser	Ile	65	70	75	80
Gln	Glu	Ala	Glu	Asn	Pro	Val	Gln	Pro	Ala	Glu	Glu	Ser	Thr	Thr	Asn	85	90	95	
Ser	Glu	Lys	Val	Ser	Pro	Asp	Thr	Ser	Ser	Lys	Asn	Thr	Gly	Glu	Val	100	105	110	
Ser	Ser	Asn	Pro	Ser	Asp	Ser	Thr	Thr	Ser	Val	Gly	Glu	Ser	Asn	Lys	115	120	125	
Pro	Glu	His	Asn	Asp	Ser	Lys	Asn	Glu	Asn	Ser	Glu	Lys	Thr	Val	Glu	130	135	140	
Glu	Val	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Val	Glu	Gly	Thr	Ser	Asn	145	150	155	160

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Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn
165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro
180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn
195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn
210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val
225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys
245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys
260 265 270

Thr Leu Glu Leu Arg Asn
275

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 709 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA	60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA	120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC	180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC	240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC	300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG	360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG	420
TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC	480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT	540
TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT	600
CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT	660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT	709

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu
1           5           10           15

Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val
          20           25           30

Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile
          35           40           45

Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala
          50           55           60

Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr
65           70           75           80

Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val
          85           90           95

Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly
          100          105          110

Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly
          115          120          125

Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser
          130          135          140

Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala
145          150          155          160

Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys
          165          170          175

Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val
          180          185          190

Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr
          195          200          205

Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala
210          215          220

Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn
225          230          235

```

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTCACGA GAAAATGGCT CTGGGACACG 60
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120
CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTTA GATGGTGAAT ACCCTCTTCA 300
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420
AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTC 480
CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAATCCTT GAAGAAGGTA AGAGTCTCAC 660
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTTGTGGTC AATAATGACA ATAAGGCAAG 720
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780
GATTAAA 787

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly
1 5 10 15
Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys
20 25 30
Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln
35 40 45
Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala
50 55 60
Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu
65 70 75 80
Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu
85 90 95

214

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser
100 105 110

Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln
115 120 125

Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr
130 135 140

Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser
145 150 155 160

Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys
165 170 175

Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala
180 185 190

Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser
195 200 205

Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile
210 215 220

Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser
225 230 235 240

Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr
245 250 255

Thr Trp Asp Lys Ile Lys
260

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG	60
TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA	120
ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA	180
TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA	240
TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACACC AAGAGTCTCC TTAAGGCAGG	300
CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT	360
ACCTGAAACT ATTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT	420
G	421

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1           5           10           15

Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
          20           25           30

Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
          35           40           45

Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
          50           55           60

Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65           70           75           80

Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
          85           90           95

Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
          100          105          110

Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
          115          120          125

Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                     331

```

(2) INFORMATION FOR SEQ ID NO:102:

09765272.012204

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1           5           10           15

Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
          20           25           30

Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
          35           40           45

Glu Ala Lys Lys Lys Val Glu Ala Glu Lys Lys Ala Lys Asp Gln
          50           55           60

Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65           70           75           80

Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
          85           90           95

Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

09765373 019004

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp	Thr	Thr	Gly	Asn	Trp	Asp	Glu	Val	Ile	Ser	Gly	Lys	Ile	Asp	Lys	
1				5					10					15		
Tyr	Lys	Asp	Pro	Asp	Ile	Pro	Thr	Val	Glu	Ser	Gln	Glu	Val	Thr	Ser	
			20					25					30			
Asp	Ser	Ser	Asp	Lys	Glu	Ile	Thr	Val	Arg	Tyr	Asp	Arg	Leu	Ser	Thr	
			35				40					45				
Pro	Glu	Lys	Pro	Ile	Pro	Gln	Pro	Asn	Pro	Glu	His	Pro	Ser	Val	Pro	
			50			55					60					
Thr	Pro	Asn	Pro	Glu	Leu	Pro	Asn	Gln	Glu	Thr	Pro	Thr	Pro	Asp	Lys	
65					70					75					80	
Pro	Thr	Pro	Glu	Pro	Gly	Thr	Pro	Lys	Thr	Glu	Thr	Pro	Val	Asn	Pro	
					85				90					95		
Asp	Pro	Glu	Val	Pro	Thr	Tyr	Glu	Thr	Gly	Lys	Arg	Glu	Glu	Leu	Pro	
			100					105					110			
Asn	Thr	Gly	Thr	Glu	Ala	Asn										
			115													

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA	60
GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT	120
TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC	180
AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA	240
GCTAACAGAT GTCTTAAAG AACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG	300
TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG	360
CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG	420
TGTAAACCAA GTAATTCCTT ATGAATATT CGCTGGTGAT GGTATGTTAA CTCGTCTATT	480
ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT	540
ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA	600

TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660
 TTATAAAGCT ACTGTTAAAG TTTACGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GGCGAAAACG TGAAGACCAA 1020
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAAACAAGC 1080
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG 1380
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTAAAAACCC 1440
 AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620
 CTTGGACAAC ATCGTAGCAA CTAAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860
 GTCAGAGGAT AAAGCTATG 1879

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser
 1 5 10 15
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu
 20 25 30

Thr Gln Ala Lys Pro Glu Gly Val Thr Gly Asn Thr Asn Ser Leu Pro
 35 40 45
 Thr Pro Thr Glu Arg Thr Glu Val Ser Glu Glu Thr Ser Pro Ser Ser
 50 55 60
 Leu Asp Thr Leu Phe Glu Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu
 65 70 75 80
 Leu Thr Asp Val Leu Lys Glu Thr Val Asp Thr Ala Asp Val Asp Gly
 85 90 95
 Thr Gln Ala Ser Pro Ala Glu Thr Thr Pro Glu Gln Val Lys Gly Gly
 100 105 110
 Val Lys Glu Asn Thr Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
 115 120 125
 Glu Lys Ala Glu Gly Lys Gly Pro Phe Thr Ala Gly Val Asn Gln Val
 130 135 140
 Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
 145 150 155 160
 Leu Lys Ala Ser Asp Asn Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys
 165 170 175
 Asn Pro Ala Leu Pro Pro Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe
 180 185 190
 Tyr Glu Val Asp Leu Asn Gly Asn Thr Val Gly Lys Gln Gly Gln Ala
 195 200 205
 Leu Ile Asp Gln Leu Arg Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr
 210 215 220
 Val Lys Val Tyr Gly Asn Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu
 225 230 235 240
 Val Ala Thr Lys Asn Val Asp Ile Asn Ile Asn Gly Leu Val Ala Lys
 245 250 255
 Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser Ile Asp
 260 265 270
 Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr
 275 280 285
 Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly
 290 295 300
 Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser
 305 310 315 320
 Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn
 325 330 335
 Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Xaa Ala Leu Asp Gly Asn
 340 345 350
 Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg Ala Xaa
 355 360 365

09765522 042201
 102270 2259260

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp
 370 375 380
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile
 385 390 395 400
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala
 405 410 415
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys
 420 425 430
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro
 435 440 445
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys
 450 455 460
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro
 465 470 475 480
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe
 485 490 495
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala
 500 505 510
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr
 515 520 525
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile
 530 535 540
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser
 545 550 555 560
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val
 565 570 575
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro
 580 585 590
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met
 595 600 605
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys
 610 615 620
 Ala Met
 625

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AAACAGGCAG ATGGTAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60
 TGA rTTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240
 GGATAAGAAA AAAGTGAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540
 CTTTGTGACT CAACACGCag CCTTTAACTa TCTTGCTTG GACTATGGGA CTC 593

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser	Asn	Gln	Lys	Gln	Ala	Asp	Gly	Lys	Leu	Asn	Ile	Val	Thr	Thr	Phe	1	5	10	15
Tyr	Pro	Val	Tyr	Glu	Phe	Thr	Lys	Gln	Val	Ala	Gly	Asp	Thr	Ala	Asn	20	25	30	
Val	Glu	Leu	Leu	Ile	Gly	Ala	Gly	Thr	Glu	Pro	His	Glu	Tyr	Glu	Pro	35	40	45	
Ser	Ala	Lys	Ala	Val	Ala	Lys	Ile	Gln	Asp	Ala	Asp	Thr	Phe	Val	Tyr	50	55	60	
Glu	Asn	Glu	Asn	Met	Glu	Thr	Trp	Val	Pro	Lys	Leu	Leu	Asp	Thr	Leu	65	70	75	80
Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala	Thr	Gly	Asp	Met	Leu	Leu	85	90	95	
Leu	Pro	Gly	Gly	Glu	Glu	Glu	Gly	Asp	His	Asp	His	Gly	Glu	Glu	100	105	110		
Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val	Trp	Leu	Ser	Pro	Val	Arg	115	120	125	
Ala	Ile	Lys	Leu	Val	Glu	His	His	Pro	Arg	His	Leu	Ser	Ala	Asp	Tyr	130	135	140	
Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn	Ala	Ala	Tyr	Ile	Glu	145	150	155	160	

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Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala
 165 170 175

Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala
 180 185 190

Leu Asp Tyr Gly Thr
 195

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTTAT GGAACTTTCT TCTTTCCAAC TCATGGGTGT	180
TCAAGAAATC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTC CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGTACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCTTTCAGC CTTCGGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGCC	660
TACTCAAAA GCCTTGTCAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT	720
GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT	780
CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA	840
TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG	900
AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT	960
ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA	1003

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly	Ile	Thr	Gly	Ser	Asn	Gly	Lys	Thr	Thr	Thr	Met	Ile	Gly	1	5	10	15		
Glu	Val	Leu	Thr	Ala	Ala	Gly	Gln	His	Gly	Leu	Leu	Ser	Gly	Asn	Ile	20	25	30	
Gly	Tyr	Pro	Ala	Ser	Gln	Val	Ala	Gln	Ile	Ala	Ser	Asp	Lys	Asp	Thr	35	40	45	
Leu	Val	Met	Glu	Leu	Ser	Ser	Phe	Gln	Leu	Met	Gly	Val	Gln	Glu	Phe	50	55	60	
His	Pro	Glu	Ile	Ala	Val	Ile	Thr	Asn	Leu	Met	Pro	Thr	His	Ile	Asp	65	70	75	80
Tyr	His	Gly	Ser	Phe	Ser	Glu	Tyr	Val	Ala	Ala	Lys	Trp	Asn	Ile	Gln	85	90	95	
Asn	Lys	Met	Thr	Ala	Ala	Asp	Phe	Leu	Val	Leu	Asn	Phe	Asn	Gln	Asp	100	105	110	
Leu	Ala	Lys	Asp	Leu	Thr	Ser	Lys	Thr	Glu	Ala	Thr	Val	Val	Pro	Phe	115	120	125	
Ser	Thr	Leu	Glu	Lys	Val	Asp	Gly	Ala	Tyr	Leu	Glu	Asp	Gly	Gln	Leu	130	135	140	
Tyr	Phe	Arg	Gly	Glu	Val	Val	Met	Ala	Ala	Asn	Glu	Ile	Gly	Val	Pro	145	150	155	160
Gly	Ser	His	Asn	Val	Glu	Asn	Ala	Leu	Ala	Thr	Ile	Ala	Val	Ala	Lys	165	170	175	
Leu	Arg	Asp	Val	Asp	Asn	Gln	Thr	Ile	Lys	Glu	Thr	Leu	Ser	Ala	Phe	180	185	190	
Gly	Gly	Val	Lys	His	Arg	Leu	Gln	Phe	Val	Asp	Asp	Ile	Lys	Gly	Val	195	200	205	
Lys	Phe	Tyr	Asn	Asp	Ser	Lys	Ser	Thr	Asn	Ile	Leu	Ala	Thr	Gln	Lys	210	215	220	
Ala	Leu	Ser	Gly	Phe	Asp	Asn	Ser	Lys	Val	Val	Leu	Ile	Ala	Gly	Gly	225	230	235	240
Leu	Asp	Arg	Gly	Asn	Glu	Phe	Asp	Glu	Leu	Val	Pro	Asp	Ile	Thr	Gly	245	250	255	
Leu	Lys	Lys	Met	Val	Ile	Leu	Gly	Gln	Ser	Ala	Glu	Arg	Val	Lys	Arg	260	265	270	
Ala	Ala	Asp	Lys	Ala	Gly	Val	Ala	Tyr	Val	Glu	Ala	Thr	Asp	Ile	Ala	275	280	285	
Asp	Ala	Thr	Arg	Lys	Ala	Tyr	Glu	Leu	Ala	Thr	Gln	Gly	Asp	Val	Val	290	295	300	
Leu	Leu	Ser	Pro	Ala	Asn	Ala	Ser	Trp	Asp	Met	Tyr	Ala	Asn	Phe	Glu				

(2) INFORMATION FOR SEQ ID NO: 111:

(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAGTTCATCG	AAGATGGTTG	GGAAGTCCAC	TATATCGGGG	ACAAGTGTGG	TATCGAACAC	60
CAAGAAATCC	TTAAGTCAGG	TTTGGATGTC	ACCTTCCATT	CTATTGCGAC	TGGAAATTG	120
CGTCGCTATT	TCTCTTGCA	AAATATGCTG	GACGTCTTCA	AAGTTGGTTG	GGGAATTGTC	180
CAATCGCTCT	TTATCATGTT	GCGACTGCGT	CCACAGACCC	TTTTTTCAAA	GGGGGGCTTT	240
GTCTCAGTAC	CGCCTGTTAT	CGCTGCGCGT	GTGTCAGGAG	TGCCTGTCTT	TATTCACGAA	300
TCTGACCTGT	CTATGGGCTT	GGCCAATAAA	ATCGCCTATA	AATTTGCGAC	TAAGATGTAT	360
TCAACCTTTG	AACAAGCTTC	GAGTTTGGCT	AAGGTTGAGC	ATGTGGGAGC	GG	412

(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser	Ser	Ser	Lys	Met	Val	Gly	Lys	Ser	Thr	Ile	Ser	Gly	Thr	Ser	Val
1			5						10					15	
Val	Ser	Asn	Thr	Lys	Lys	Ser	Leu	Ser	Gln	Val	Trp	Met	Ser	Pro	Ser
		20						25					30		
Ile	Leu	Leu	Arg	Leu	Glu	Asn	Cys	Val	Ala	Ile	Ser	Leu	Gly	Lys	Ile
	35						40					45			
Cys	Trp	Thr	Ser	Ser	Lys	Leu	Val	Gly	Glu	Leu	Ser	Asn	Arg	Ser	Leu
	50					55					60				
Ser	Cys	Cys	Asp	Cys	Val	His	Arg	Pro	Phe	Phe	Gln	Arg	Gly	Ala	Leu
65				70						75					80
Ser	Gln	Tyr	Arg	Leu	Leu	Ser	Leu	Arg	Val	Cys	Gln	Glu	Cys	Leu	Ser
			85						90					95	
Leu	Phe	Thr	Asn	Leu	Thr	Cys	Leu	Trp	Ala	Trp	Pro	Ile	Lys	Ser	Pro

225

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val
 115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg
 130 135

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC 60
 AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT 120
 GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA 180
 TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA 240
 AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG 300
 AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG 360
 TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC 420
 GTTTGATACA ATAATGAAGG TGACTACAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA 480
 TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC 540
 GAAT 544

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr
 1 5 10 15
 Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser
 20 25 30
 Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys
 35 40 45
 Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

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(2) INFORMATION FOR SEQ ID NO: 115:

(A) LENGTH: 1267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG	GGGCACAAGG	TTCAGGGATC	AGATGTTGAA	AAGTACTACT	TTACCCAACG	60
CGGTCTTGAG	CAGGCAGGAA	TTACCATTCT	TCCTTTTGAT	GAAAAAAATC	TAGACGGTGA	120
TATGGAAATT	ATCGCTGGAA	ATGCCTTTCTG	TCCAGATAAC	AACGTCGAAA	TTGCCTATGC	180
GGACCAAAAT	GGTATCAGCT	ACAAACGTTA	CCATGAGTTT	CTAGGTAGCT	TTATGCGTGA	240
CTTTGTTAGC	ATGGGAGTAG	CAGGAGCACA	TGGAAAAACT	TCAACGACAG	GTATGTTGTC	300
TCATGTCTTG	TCTCACATTA	CAGATACCAG	CTTCTTGATT	GGAGATGGGA	CAGGTCGTGG	360
TTCGGCCAAT	GCCAAATATT	TTGTCTTTGA	ATCTGACGAA	TATGAGCGTC	ACTTCATGCC	420
TTACCACCCA	GAATACTCTA	TTATCACCAA	CATTGACTTT	GACCATCCAG	ATTATTTTAC	480
AAGTCTCGAG	GATGTTTTTA	ATGCCTTTAA	CGACTATGCC	AAACAAATCA	CCAAGGGTCT	540
TTTTGTCTAT	GGTGAAGATG	CTGAATTGCG	TAAGATTACG	TCTGATGCAC	CAATTTATTA	600
TTATGGTTTT	GAAGCTGAAG	GCAATGACTT	TGTAGCTAGT	GATCTTCTTC	GTTCAATAAC	660
TGGTTCAACC	TTCACCGTTC	ATTTCCGTGG	ACAAAACCTG	GGGCAATTCC	ACATTCCAAC	720
CTTTGGTCGT	CACAAATATCA	TGAATGCGAC	AGCCGTTATT	GGTCTTCTTT	ACACAGCAGG	780

ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCACC ATCCAACAGA 900
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140
 TGTGAAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260
 TGTTCAA 1267

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

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165	170	175
Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile		
180	185	190
Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn		
195	200	205
Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe		
210	215	220
Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr		
225	230	235
Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu		
245	250	255
Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr		
260	265	270
Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr		
275	280	285
Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr		
290	295	300
Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val		
305	310	315
Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe		
325	330	335
Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr		
340	345	350
Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu		
355	360	365
Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val		
370	375	380
Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala		
385	390	395
Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn		
405	410	415
Leu Thr Ser Asn Val Gln		
420		

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT

GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGA TAGCAT	120
GGGAGTTCAA TTGTTGCCGG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACC GGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC	960
GGCTTTAGAG GTC ACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCG TAGAACTAA	1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AAC TGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTC AAT TAGAGTATAA	1500
GAAAATAGAG ATTAAAGATA TTGATT CAGT AGAATTATAC GGTAAAGAAA ATGATCGTTA	1560
TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT	1620
GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	1680
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA	1740
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	1800
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	1860
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	1920

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGACAAAA TCGTATGCCA TTTATGATTT 1980
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040
 TGTTCCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520
 TGTTCATACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCCT ATGGTAACAA 2820
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 2880
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAACAG 3000
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120
 C 3121

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
 1 5 10 15
 Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
 20 25 30
 His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
 35 40 45

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Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
 50 55 60
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
 65 70 75 80
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
 85 90 95
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
 100 105 110
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
 115 120 125
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
 130 135 140
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
 145 150 155 160
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
 165 170 175
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
 180 185 190
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
 195 200 205
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
 210 215 220
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
 225 230 235 240
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
 245 250 255
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
 260 265 270
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
 275 280 285
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
 290 295 300
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
 305 310 315 320
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
 325 330 335
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
 340 345 350
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
 355 360 365
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
 370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
 385 390 395 400
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
 405 410 415
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
 420 425 430
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
 435 440 445
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
 450 455 460
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
 465 470 475 480
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
 485 490 495
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
 500 505 510
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
 515 520 525
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
 530 535 540
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
 545 550 555 560
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
 565 570 575
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
 580 585 590
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
 595 600 605
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
 610 615 620
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
 625 630 635 640
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
 645 650 655
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
 660 665 670
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
 675 680 685
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
 690 695 700
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
 705 710 715 720

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Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys
725 730 735

Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile
740 745 750

Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val
755 760 765

Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly
770 775 780

Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val
785 790 795 800

Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly
805 810 815

Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser
820 825 830

Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala
835 840 845

Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala
850 855 860

Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val
865 870 875 880

Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu
885 890 895

Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu
900 905 910

Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe
915 920 925

Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr
930 935 940

Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp
945 950 955 960

Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys
965 970 975

Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr
980 985 990

Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr
995 1000 1005

Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr
1010 1015 1020

Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn
1025 1030 1035 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT	60
GGTTTCTAAA AGGGAAAATG GAAAGAAACG ACTTGTTTCAT TTTCTGCTGT TGACTAGCAT	120
GGGAGTTCAA TTGTTGCCCG CCAGTGCTTT TGGGTTGACC AGCCAGATTT TATCTGCCTA	180
TAATAGTCAG CTTTCTATCG GAGTCGGGGA ACATTTACCA GAGCCTCTGA AAATCGAAGG	240
TTATCAATAT ATTGGTTATA TCAAACTAA GAAACAGGAT AATACAGAGC TTTCAAGGAC	300
AGTTGATGGG AAATACTCTG CTCAAAGAGA TAGTCAACCA AACTCTACAA AAACATCAGA	360
TGTAGTTCAT TCAGCTGATT TAGAATGGAA CCAAGGACAG GGGAAGGTTA GTTTACAAGG	420
TGAAGCATCA GGGGATGATG GACTTTCAGA AAAATCTTCT ATAGCAGCAG ACAATCTATC	480
TTCTAATGAT TCATTGCGAA GTCAAGTTGA GCAGAATCCG GATCACAAAG GAGAATCTGT	540
AGTTTCGACCA ACAGTGCCAG AACAAGGAAA TCCTGTGTCT GCTACAACGG TGCAGAGTGC	600
GGAAGAGGAA GTATTGGCGA CGACAAATGA TCGACCAGAG TATAAACTTC CATTTGGAAAC	660
CAAAGGCACG CAAGAACCCG GTCATGAGGG TGAAGCCGCA GTCCGTGAAG ACTTACCAGT	720
CTACACTAAG CCACTAGAAA CCAAAGGTAC ACAAGGACCC GGACATGAAG GTGAAGCTGC	780
AGTTTCGCGAG GAAGAACCAG CTTACACAGA ACCGTTAGCA ACGAAAGGCA CGCAAGAGCC	840
AGGTCATGAG GGCAAAGCTA CAGTCCGCGA AGAGACTCTA GAGTACACGG AACCGGTAGC	900
GACAAAAGGC ACACAAGAAC CCGAACATGA GGGCGAaCGG sCAGTAGAAG AAGAACTTCC	960
GGCTTTAGAG GTCACTACAC GAAATAGAAC GGAAATCCAG AATATTCCTT ATACAACAGA	1020
AGAAATTCAG GATCCAACAC TTCTGAAAAA TCGTCGTAAG ATTGAACGAC AAGGGCAAGC	1080
AGGGACACGT ACAATTCAAT ATGAAGACTA CATCGTAAAT GGTAATGTCTG TAGAAACTAA	1140
AGAAGTGTCA CGAACTGAAG TAGCTCCGGT CAACGAAGTC GTTAAAGTAG GAACACTTGT	1200
GAAAGTTAAA CCTACAGTAG AAATTACAAA CTTAACAAAA GTTGAGAACA AAAAATCTAT	1260
AACTGTAAGT TATAACTTAA TAGACACTAC CTCAGCATAT GTTTCTGCAA AAACGCAAGT	1320
TTTCCATGGA GACAAGCTAG TTAAAGAGGT GGATATAGAA AATCCTGCCA AAGAGCAAGT	1380
AATATCAGGT TTAGATTACT ACACACCGTA TACAGTTAAA ACACACCTAA CTTATAATTT	1440
GGGTGAAAAT AATGAGGAAA ATACTGAAAC ATCAACTCAA GATTTCCAAT TAGAGTATAA	1500
GAAAATAGAG ATTAAAGATA TTGATTCAGT AGAATTATAC GGTAAGAAA ATGATCGTTA	1560
TCGTAGA	1567

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(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

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Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
1           5           10           15

Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
          20           25           30

His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
          35           40           45

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
          50           55           60

Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
65           70           75           80

Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
          85           90           95

Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
          100          105          110

Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
          115          120          125

Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
          130          135          140

Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
145          150          155          160

Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
          165          170          175

Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
          180          185          190

Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
          195          200          205

Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
          210          215          220

Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
225          230          235          240

Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
          245          250          255

Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

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236

260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg
515 520

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA 120
 TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA 180
 CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC 240
 ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC 300
 TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG 360
 TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 420
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTGG ATATTAAAC 480
 TGTTTCTGCT GATAGTAAAG AAAATGTCTG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 540
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 600
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 660
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 720
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 780
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 840
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 900
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 960
 TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 1020
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 1080
 TGCTGATTAT GGAATCACAG TAACCTCTGA TGATACTGGG CAAGATTTAA AACGTAATCT 1140
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 1200
 CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA 1260
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA 1320
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 1380
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 1440
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 1500
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 1560
 C 1561

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	1	5	10	15
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	20	25	30	
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	35	40	45	
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	50	55	60	
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	65	70	75	80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	85	90	95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	100	105	110	
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	115	120	125	
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	130	135	140	
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	145	150	155	160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	165	170	175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	180	185	190	
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	195	200	205	
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	210	215	220	
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	225	230	235	240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	245	250	255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	260	265	270	
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	275	280	285	
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	290	295	300	
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	305	310	315	320

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Val Ile Thr Gly Asp Gln Tyr Ala Ala Ala Asp Val Lys Asn Ala Ser
325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser
340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr
355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp
370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser
385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His
405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu
420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn
435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn
450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser
465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro
485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
500 505 510

Asp Leu Gln Asn Val Thr Leu Asn
515 520

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 850 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GACACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA	360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480
 TACTTCAATT GATGAAAGTA TGC GTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTA ACTACCG 600
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720
 TGATTGGGAT CTTGCGCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTTT 840
 CAAAAATCGT 850

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe	Gly	Phe	Glu	Gly	Ser	Lys	Arg	Gly	Gln	Phe	Ala	Val	Glu	Gly	Ile	1	5	10	15
Asn	Gln	Leu	Arg	Glu	His	Val	Asp	Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	20	25	30	
Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys	Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	35	40	45	
Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg	Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	50	55	60	
Leu	Ile	Thr	Asn	Pro	Gly	Leu	Ile	Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	65	70	75	80
Thr	Val	Met	Ala	Asn	Lys	Gly	Asn	Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	85	90	95	
Ser	Gly	Glu	Glu	Arg	Val	Val	Glu	Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	100	105	110	
Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp	Gly	Ala	Glu	Asp	Val	Ile	Val	Asn	115	120	125	
Val	Thr	Gly	Gly	Leu	Asp	Leu	Thr	Leu	Ile	Glu	Ala	Glu	Glu	Ala	Ser	130	135	140	
Gln	Ile	Val	Asn	Gln	Ala	Gly	Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly		145	150	155	160
Thr	Ser	Ile	Asp	Glu	Ser	Met	Arg	Asp	Glu	Ile	Arg	Val	Thr	Val	Val	165	170	175	

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Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln
180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser
195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro
210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly
225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val
245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp
260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg
275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAATA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTTGA TTCCCTTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG	900

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TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCCTCACA ACTGGTCCTA TCATTGGTTA 960
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCCTCTAA ATTACCCAAT 1020
 TGAAAACATAT GTCAAACGAG TAAAAAGCGA A 1051

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr Tyr Leu Ser Arg Glu Ser Asp Leu Glu Val Thr Val Phe Asp His
 1 5 10 15
 Glu Gln Gly Gln Ala Thr Lys Ala Ala Ala Gly Ile Ile Ser Pro Trp
 20 25 30
 Phe Ser Lys Arg Arg Asn Lys Ala Trp Tyr Lys Met Ala Arg Leu Gly
 35 40 45
 Ala Asp Phe Tyr Val Asp Leu Leu Ala Asp Leu Glu Lys Ser Gly Gln
 50 55 60
 Glu Ile Asp Phe Tyr Gln Arg Ser Gly Val Phe Leu Leu Lys Lys Asp
 65 70 75 80
 Glu Ser Asn Leu Glu Glu Leu Tyr Gln Leu Ala Leu Gln Arg Arg Glu
 85 90 95
 Glu Ser Pro Leu Ile Gly Gln Leu Ala Ile Leu Asn Gln Ala Ser Ala
 100 105 110
 Asn Glu Leu Phe Pro Gly Leu Gln Gly Phe Asp Arg Leu Leu Tyr Ala
 115 120 125
 Ser Gly Gly Ala Arg Val Asp Gly Gln Leu Leu Val Thr Arg Leu Leu
 130 135 140
 Glu Val Ser His Val Lys Leu Val Lys Glu Lys Val Thr Leu Thr Pro
 145 150 155 160
 Leu Ala Ser Gly Tyr Gln Ile Gly Glu Glu Glu Phe Glu Gln Val Ile
 165 170 175
 Leu Ala Thr Gly Ala Trp Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr
 180 185 190
 Glu Val Asp Val Arg Pro Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu
 195 200 205
 Ala Gln Asp Met Glu Asp Tyr Pro Val Val Met Pro Glu Gly Glu Trp
 210 215 220
 Asp Leu Ile Pro Phe Ala Gly Gly Lys Leu Ser Leu Gly Ala Thr His

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(2) INFORMATION FOR SEO ID NO: 127:

(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAGGTCAAA	AGTCAGACCG	CTAAGAAAGT	GCTAGAAAAG	ATTGGAGCTG	ACTCGGTTAT	60
CTCGCCAGAG	TATGAAATGG	GGCAGTCTCT	AGCACAGACC	ATTCTTTTCC	ATAATAGTGT	120
TGATGTCTTT	CAGTTGGATA	AAAATGTGTC	TATCGTGGAG	ATGAAAATTC	CTCAGTCTTG	180
GGCAGGTCAA	AGTCTGAGTA	AATTAGACCT	CCGTGGCAA	TACAATCTGA	ATATTTTGGG	240
TTTCCGAGAG	CAGGAAAATT	CCCATTGGA	TGTTGAATTT	GGACCAGATG	ACCTCTTGAA	300
AGCAGATACC	TATATTTTGG	CAGTCATCAA	CAACCAGTAT	TTGGATACCC	TA	352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala
1 5 10 15

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln
 20 25 30
 Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn
 35 40 45
 Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser
 50 55 60
 Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly
 65 70 75 80
 Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp
 85 90 95
 Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln
 100 105 110
 Tyr Leu Asp Thr Leu
 115

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA	60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT	120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG	180
TGCCTACTTG AAAATTCTTG AAAGTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT	240
GTCTTTG	247

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser
 1 5 10 15
 Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His
 20 25 30
 Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

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	35		40		45	
Lys	Val	Val	Asp	Ser	Asp	Asp
50					55	
						60
Ile	Leu	Glu	Thr	Cys	Arg	Asn
65					70	
						75
						80
Ser	Leu					

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA	60
ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC	120
TGAAAAAGCC TTA CTGATT TGCCTCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA	180
GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT	240
CCTGCCTCAA GCTGAACTTA AATTCCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT	300
TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCCAAGCT TACAATCTTT	360
TGCACCAGAT AAACCAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA	420
AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT	480
TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT	540
TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC	600
ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT	660
ATCTTTCCGA GAACTATGGG AACAAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTCC	720
TTTAGGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT	780
GCTAGTTGCA GGTTCACCGG GTTCAGGGAA GTCAGTAGCA GTTAACGGCA TTATTGCTAG	840
CATTCTCATG AAGGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT	900
TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG	960
CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT	1020
TGCCAAGGTG GGAGTTCGGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATTC	1080
CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCATTGTC GTGATTGTGG ATGAGTTGGC	1140
TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA	1200

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GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440
 TGACGATGTT GAGCGCATTG TGAACCTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740
 ACAA 1744

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 581 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg Gly Phe Ala Lys Trp Trp Glu Gly His Glu Arg Arg Lys Glu Glu
 1 5 10 15
 Arg Phe Val Lys Gln Glu Glu Lys Ala Arg Gln Lys Ala Glu Lys Glu
 20 25 30
 Ala Arg Leu Glu Gln Glu Glu Thr Glu Lys Ala Leu Leu Asp Leu Pro
 35 40 45
 Pro Val Asp Met Glu Thr Gly Glu Ile Leu Thr Glu Glu Ala Val Gln
 50 55 60
 Asn Leu Pro Pro Ile Pro Glu Glu Lys Trp Val Glu Pro Glu Ile Ile
 65 70 75 80
 Leu Pro Gln Ala Glu Leu Lys Phe Pro Glu Gln Glu Asp Asp Ser Asp
 85 90 95
 Asp Glu Asp Val Gln Val Asp Phe Ser Ala Lys Glu Ala Leu Glu Tyr
 100 105 110
 Lys Leu Pro Ser Leu Gln Leu Phe Ala Pro Asp Lys Pro Lys Asp Gln
 115 120 125
 Ser Lys Glu Lys Lys Ile Val Arg Glu Asn Ile Lys Ile Leu Glu Ala
 130 135 140
 Thr Phe Ala Ser Phe Gly Ile Lys Val Thr Val Glu Arg Ala Glu Ile
 145 150 155 160

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Gly Pro Ser Val Thr Lys Tyr Glu Val Lys Pro Ala Val Gly Val Arg
 165 170 175
 Val Asn Arg Ile Ser Asn Leu Ser Asp Asp Leu Ala Leu Ala Leu Ala
 180 185 190
 Ala Lys Asp Val Arg Ile Glu Ala Pro Ile Pro Gly Lys Ser Leu Ile
 195 200 205
 Gly Ile Glu Val Pro Asn Ser Asp Ile Ala Thr Val Ser Phe Arg Glu
 210 215 220
 Leu Trp Glu Gln Ser Gln Thr Lys Ala Glu Asn Phe Leu Glu Ile Pro
 225 230 235 240
 Leu Gly Lys Ala Val Asn Gly Thr Ala Arg Ala Phe Asp Leu Ser Lys
 245 250 255
 Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly Lys Ser Val
 260 265 270
 Ala Val Asn Gly Ile Ile Ala Ser Ile Leu Met Lys Ala Arg Pro Asp
 275 280 285
 Gln Val Lys Phe Met Met Val Asp Pro Lys Met Val Glu Leu Ser Val
 290 295 300
 Tyr Asn Asp Ile Pro His Leu Leu Ile Pro Val Val Thr Asn Pro Arg
 305 310 315 320
 Lys Ala Ser Lys Ala Leu Gln Lys Val Val Asp Glu Met Glu Asn Arg
 325 330 335
 Tyr Glu Leu Phe Ala Lys Val Gly Val Arg Asn Ile Ala Gly Phe Asn
 340 345 350
 Ala Lys Val Glu Glu Phe Asn Ser Gln Ser Glu Tyr Lys Gln Ile Pro
 355 360 365
 Leu Pro Phe Ile Val Val Ile Val Asp Glu Leu Ala Asp Leu Met Met
 370 375 380
 Val Ala Ser Lys Glu Val Glu Asp Ala Ile Ile Arg Leu Gly Gln Lys
 385 390 395 400
 Ala Arg Ala Ala Gly Ile His Met Ile Leu Ala Thr Gln Arg Pro Ser
 405 410 415
 Val Asp Val Ile Ser Gly Leu Ile Lys Ala Asn Val Pro Ser Arg Val
 420 425 430
 Ala Phe Ala Val Ser Ser Gly Thr Asp Ser Arg Thr Ile Leu Asp Glu
 435 440 445
 Asn Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp Met Leu Phe Lys Pro
 450 455 460
 Ile Asp Glu Asn His Pro Val Arg Leu Gln Gly Ser Phe Ile Ser Asp
 465 470 475 480
 Asp Asp Val Glu Arg Ile Val Asn Phe Ile Lys Thr Gln Ala Asp Ala
 485 490 495

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Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly
 500 505 510
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala
 515 520 525
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln
 530 535 540
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu
 545 550 555 560
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg
 565 570 575
 Lys Val Leu Gln Gln
 580

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGACTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAAA CCCATGTCTT ATCAAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTA CTTGAAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAA	829

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu
 1 5 10 15
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr
 20 25 30
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu
 35 40 45
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr
 50 55 60
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His
 65 70 75 80
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln
 85 90 95
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala
 100 105 110
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile
 115 120 125
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu
 130 135 140
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr
 145 150 155 160
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln
 165 170 175
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp
 180 185 190
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln
 195 200 205
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu
 210 215 220
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys
 225 230 235 240
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu
 245 250 255
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly
 260 265 270
 Leu Leu Lys Lys
 275

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA      60
AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT      120
CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG      180
AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGAATTGATG GATATCACAG ACGAAAAGGC      240
TGTTCCACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTACTATCGC      300
TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCGA      360
AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGTGAA AAACCAGCTC CAGAGGACGC      420
TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT      480
CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTACAGCTG ACAGATGCAA TCGACACCCT      540
CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GTCGTTACG ATGTCGGAGA      600
CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA      660
TGATTTGAAG AATTACCTCA TCCAATTGG AAAAGAATTG ACTGAGAAGG AA              712

```

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn
1           5           10           15
Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr
          20           25           30
Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu
          35           40           45
Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe
          50           55           60
Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala
          65           70           75           80

```

Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala
85 90 95

Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr
100 105 110

Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val
115 120 125

Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu
130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu
145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala
165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys
180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser
195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn
210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu
225 230 235

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACTTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCGAAGAC ATGCAGCGTG CTGGTCGCCT 360

GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTATCAAA GGCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	
1				5					10					15		
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	
			20					25					30			
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	
			35				40					45				
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	
			50			55					60					
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	
65					70					75					80	
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	
				85					90					95		
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	
			100					105					110			
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	
			115				120					125				
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	
			130			135					140					
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	
145					150					155					160	
Thr	Cys	His	Thr	His	Gly	Thr										
					165											

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAACCC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTTGC	AAAAAGGTTT	GGCTTATGAT	GTAAAGATT	CAGATGACAA	240

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ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAGAA ATTACAAAAC AAATTGATTT      300
TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAAACTC TTAAATCTCT      360
AAATGATCTT GTTGATAAAT ATCAAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA      420
AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG      480
TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC      540
TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA      600
TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC      660
AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA      720
AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGGA ACTTTGGTGG      780
CGGCATTGCA GAACCTAGTC AACGC                                             805

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Ile Val Gln Leu Glu Lys Asp Ser Lys Ser Asp Lys Glu Gln Val Asp
1           5           10           15
Lys Leu Phe Glu Ser Phe Asp Ala Ser Ser Asp Glu Ser Ile Ser Lys
20           25           30
Leu Lys Glu Leu Ser Glu Thr Ser Leu Lys Thr Asp Ala Gly Lys Asp
35           40           45
Tyr Leu Asn Asn Lys Val Lys Glu Ser Ser Lys Ala Ile Val Asp Phe
50           55           60
His Leu Gln Lys Gly Leu Ala Tyr Asp Val Lys Asp Ser Asp Asp Lys
65           70           75           80
Phe Lys Asp Lys Ala Thr Leu Glu Thr Asn Val Lys Glu Ile Thr Lys
85           90           95
Gln Ile Asp Phe Ile Lys Lys Val Asp Glu Thr Phe Lys Gln Glu Asn
100          105          110
Leu Glu Glu Thr Leu Lys Ser Leu Asn Asp Leu Val Asp Lys Tyr Gln
115          120          125
Lys Gln Ile Glu Leu Leu Lys Lys Glu Glu Glu Lys Ala Ala Glu Lys
130          135          140
Ala Ala Glu Lys Ala Lys Glu Ser Ser Ser Gln Ser Asn Ser Ser Gly
145          150          155          160

```

(2) INFORMATION FOR SEQ ID NO: 141:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

(2) INFORMATION FOR SEQ ID NO:142:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val
1 5 10 15

Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn
20 25 30

Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu
35 40 45

Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala
 50 55 60

Asn Arg Lys Val Asn Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT 60
 TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAAA AGACTAGTCT 120
 GAACTTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT 180
 TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC 240
 TAAGGTTGAA TTTCAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG 300
 AAAAATTAAA CGCATTAAGG AAACAAAAAA T 331

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe
 1 5 10 15
 Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val
 20 25 30
 Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser
 35 40 45
 Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser
 50 55 60
 Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala
 65 70 75 80
 Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr
 85 90 95
 Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn
 100 105 110

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 T02220

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAATC TTGCAAAGG AAGAAGTCTT      60
GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA    120
GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT    180
GGCAATCAAA GAGCCA                                     196

```

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys
1           5           10           15
Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn
          20           25           30
Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys
          35           40           45
Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu
          50           55           60
Pro
65

```

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147: - - - - -

```

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGAAC AACTTGAGGT      60

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AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240
 TCAACTGGTT CGCTTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300
 TGTGGAAAAA GAAAAAAGT 319

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp
 1 5 10 15
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly
 20 25 30
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys
 35 40 45
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr
 50 55 60
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn
 65 70 75 80
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu
 85 90 95
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT 60
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTTAA 120
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180
 TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240

AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300

GCCTGAAAAG AAAGAGAATT CA 322

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn	Arg	Gln	Val	Ala	His	Tyr	Gln	Asp	Tyr	Ala	Leu	Asn	Lys	Glu	Lys	
1				5					10					15		
Leu	Val	Ala	Phe	Ala	Met	Ala	Lys	Arg	Thr	Lys	Asp	Lys	Val	Glu	Gln	
		20						25					30			
Glu	Ser	Gly	Glu	Gln	Phe	Phe	Asn	Leu	Gly	Gln	Val	Ser	Tyr	Gln	Asn	
		35					40					45				
Lys	Lys	Thr	Gly	Leu	Val	Thr	Arg	Val	Arg	Thr	Asp	Lys	Ser	Gln	Tyr	
		50				55					60					
Glu	Phe	Leu	Phe	Pro	Ser	Val	Lys	Ile	Lys	Glu	Glu	Lys	Arg	Asp	Lys	
65					70					75					80	
Lys	Glu	Glu	Val	Ala	Thr	Asp	Ser	Ser	Glu	Lys	Val	Glu	Lys	Lys	Lys	
			85						90					95		
Ser	Glu	Glu	Lys	Pro	Glu	Lys	Lys	Glu	Asn	Ser						
			100					105								

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC	TGGCAATATA	TCCCGTTTCC	ATCTAAAGGT	AGTACAATTG	GTCCTTACCC	60
AAATGGTATC	AGATTAGAAG	GTTTTCCAAA	GTCAGAGTGG	TACTACTTCG	ATAAAAATGG	120
AGTGCTACAA	GAGTTTGTTG	GTTGGAAAAC	ATTAGAGATT	AAACTAAAG	ACAGTGTTGG	180
AAGAAAGTAC	GGGGAAAAAC	GTGAAGATTC	AGAAGATAAA	GAAGAGAAGC	GTTATTATAC	240
GAAGTATTAC	TTTAATCAAA	ATCATTCCTT	AGAGACAGGT	TGGCTTTATG	ATCAGTCTAA	300
CTGGTATTAT	CTAGCTAAGA	CGGAAATTAA	TGGAGAAAAC	TACCTTGGTG	GTGAAAGACG	360

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TCGGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTTCCT CAGGAGCAAT 480
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540
 TATGAAAACA GGTGCGCAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600
 TATGGCAACT GGTGCGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780
 TCGG 784

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val Val Gly Trp Gln Tyr Ile Pro Phe Pro Ser Lys Gly Ser Thr Ile
 1 5 10 15
 Gly Pro Tyr Pro Asn Gly Ile Arg Leu Glu Gly Phe Pro Lys Ser Glu
 20 25 30
 Trp Tyr Tyr Phe Asp Lys Asn Gly Val Leu Gln Glu Phe Val Gly Trp
 35 40 45
 Lys Thr Leu Glu Ile Lys Thr Lys Asp Ser Val Gly Arg Lys Tyr Gly
 50 55 60
 Glu Lys Arg Glu Asp Ser Glu Asp Lys Glu Glu Lys Arg Tyr Tyr Thr
 65 70 75 80
 Asn Tyr Tyr Phe Asn Gln Asn His Ser Leu Glu Thr Gly Trp Leu Tyr
 85 90 95
 Asp Gln Ser Asn Trp Tyr Tyr Leu Ala Lys Thr Glu Ile Asn Gly Glu
 100 105 110
 Asn Tyr Leu Gly Gly Glu Arg Arg Ala Gly Trp Ile Asn Asp Asp Ser
 115 120 125
 Thr Trp Tyr Tyr Leu Asp Pro Thr Thr Gly Ile Met Gln Thr Gly Trp
 130 135 140
 Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
 145 150 155 160
 Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp His
 165 170 175
 Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp

260

	180		185		190
Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp					
195		200		205	
Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr					
210		215		220	
Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly					
225		230		235	240
Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn					
	245		250		255
Gly Glu Trp Val Arg					
260					

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTTG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT	600
TTATCTCAAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

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TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTTTTAA 1380
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCATA GTGCCCTAGA 1440
 AAGTAAGTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp
 1 5 10 15
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val
 20 25 30
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln
 35 40 45
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys
 50 55 60
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly
 65 70 75 80
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser
 85 90 95
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser
 100 105 110
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile
 115 120 125
 Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala
 130 135 140

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Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe
 145 150 155 160
 Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln
 165 170 175
 Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp
 180 185 190
 Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile
 195 200 205
 Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr
 210 215 220
 Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys
 225 230 235 240
 Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu
 245 250 255
 Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly
 260 265 270
 Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly Ser
 275 280 285
 Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala Tyr
 290 295 300
 Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly Glu
 305 310 315 320
 Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys Asp
 325 330 335
 Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu Ser
 340 345 350
 Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys Asp
 355 360 365
 Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr Val
 370 375 380
 Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met Glu
 385 390 395 400
 Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly Phe
 405 410 415
 Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr Asn
 420 425 430
 Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile Asn
 435 440 445
 Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu Glu
 450 455 460
 His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu Glu
 465 470 475 480

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(2) INFORMATION FOR SEO ID NO: 155:

(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTTGCAGAT	GATTCTGAAG	GATGGCAGTT	TGTCCAAGAA	AATGGTAGAA	CCTACTACAA	60
AAAGGGGGAT	CTAAAAGAAA	CCTACTGGAG	AGTGATAGAT	GGGAAGTACT	ATTATTTTGA	120
TCCTTTATCC	GGAGAGATGG	TTGTCTGGCTG	GCAATATATA	CCTGCTCCAC	ACAAGGGGGT	180
TACGATTGGT	CCTTCTCCAA	GAATAGAGAT	TGCTCTTAGA	CCAGATTGGT	TTTATTTTGG	240
TCAAGATGGT	GTATTACAAG	AATTTGTTGG	CAAGCAAGTT	TTAGAAGCAA	AAACTGCTAC	300
GAATACCAAC	AAACATCATG	GGGAAGAATA	TGATAGCCAA	GCAGAGAAAC	GAGTCTATTA	360
TTTTGAAGAT	CAGCGTAGTT	ATCATACTTT	AAAAACTGGT	TGGATTTATG	AAGAGGGTCA	420
TTGGTATTAT	TTACAGAAGG	ATGGTGGCTT	TGATTTCGCGC	ATCAACAGAT	TGACGGTTGG	480
AGAGCTAGCA	CGTGGTTGGG	TTAAGGATTA	CCCTCTTACG	TATGATGAAG	AGAAGCTAAA	540
AGCAGCTCCA	TGGTACTATC	TAAATCCAGC	AACTGGCATT	ATGCAAACAG	GTTGGCAATA	600
TCTAGGTAAT	AGATGGTACT	ACCTCCATTC	GTCAGGAGCT	ATGGCAACTG	GCTGGTATAA	660
GGAAGGCTCA	ACTTGGTACT	ATCTAGATGC	TGAAAATGGT	GATATGAGAA	CTGGCTGGCA	720
AAACCTTGGG	AACAAATGGT	ACTATCTCCG	TTCATCAGGA	GCTATGGCAA	CTGGTTGGTA	780
TCAGGAAAGT	TCGACTTGGT	ACTATCTAAA	TGCAAGTAAT	GGAGATATGA	AAACAGGCTG	840
GTTCCAAGTC	AATGGTAACT	GGTACTATGC	CTATGATTCA	GGTGCTTTAG	CTGTTAATAC	900
CACAGTAGGT	GGTTACTACT	TAAACTATAA	TGGTGAATGG	GTTAAG		946

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
1           5           10           15

Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
          20           25           30

Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
          35           40           45

Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
          50           55           60

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
65           70           75           80

Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
          85           90           95

Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
          100          105          110

Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
          115          120          125

His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
          130          135          140

Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
145          150          155          160

Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
          165          170          175

Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
          180          185          190

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
          195          200          205

Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
          210          215          220

Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
225          230          235          240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
          245          250          255

Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
          260          265          270

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Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp
 275 280 285

Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly
 290 295 300

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG	60
TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA	120
TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG	180
TGAATGGATT TTTGACAACT ACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA	240
CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCCAAA	300
CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA	360
TGCTCATCAA GAATGGCAAT TGATTGGAAA TAAGTGGTAC TACTTCAAGA AGTGGGGTTA	420
CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA	480
AAATGAATGG CTSCATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA	540
CTTATGCTAA CCAAGAGTGG CAAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG	600
GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG	660
CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGGCCTCT GGTGAGCTCA	720
AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TGTAAGCGC TATTTCTTTA	780
ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC	840
ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA	900
TTGTTTCGTCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GGCGCATAAC ATTAAGGAGT	960
TAAACCGTCT GGGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG	1020
ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT	1080
CTTACCCTAT CTATTATGAT GTTGAGAATT GGAATATGT AAATAAGAGC AAGAGAGCTC	1140
CAAGTGATAC AGGCACTTGG GTTAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG	1200
CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC	1260

(2) INFORMATION FOR SEQ ID NO:158:

(A) LENGTH: 471 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr
1			5						10					15	
Thr	Ala	Ser	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln
		20						25					30		
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp
	35					40					45				
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe
	50					55					60				
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr
65				70					75						80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr
			85						90					95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe
			100					105					110		
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile
	115						120					125			
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser
	130					135					140				
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln
145				150						155					160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys
			165						170					175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys
			180					185					190		
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln
	195						200					205			
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val
	210					215					220				
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys

(2) INFORMATION FOR SEQ ID NO: 159:

(A) LENGTH: 1924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCG AAAAACTTTC 60

ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA 120

AACGGCTAAA AAGAAAGCAG AAGACGCTCA GAAAAAGTAT GAAGATGATC AGAAGAGAAC 180
TGAGGAGAAA GCTCGAAAAG AAGCAGAAGC ATCTCAAAAA TTGAATGATG TGGCGCTTGT 240
TGTTCAAAAT GCATATAAAG AGTACCGAGA AGTTCAAAAT CAACGTAGTA AATATAAATC 300
TGACGCTGAA TATCAGAAAA AATTAACAGA GGTCTGACTCT AAAATAGAGA AGGCTAGGAA 360
AGAGCAACAG GACTTGCAAA ATAAATTTAA TGAAGTAAGA GCAGTTGTAG TTCCTGAACC 420
AAATGCGTTG GCTGAGACTA AGAAAAAAGC AGAAGAAGCT AAAGCAGAAG AAAAAGTAGC 480
TAAGAGAAAA TATGATTATG CAACTCTAAA GGTAGCACTA GCGAAGAAAAG AAGTAGAGGC 540
TAAGGAACTT GAAATTGAAA AACTTCAATA TGAAATTTCT ACTTTGGAAC AAGAAGTTGC 600
TACTGCTCAA CATCAAGTAG ATAATTTGAA AAAACTTCTT GCTGGTGCGG ATCCTGATGA 660
TGGCACAGAA GTTATAGAAG CTAAATTTAA AAAAGGAGAA GCTGAGCTAA ACGCTAAACA 720
AGCTGAGTTA GCAAAAAAAC AAACAGAACT TGAAAAACTT CTTGACAGCC TTGATCCTGA 780
AGGTAAGACT CAGGATGAAT TAGATAAAGA AGCAGAAGAA GCTGAGTTGG ATAAAAAAGC 840
TGATGAACTT CAAAATAAAG TTGCTGATTT AGAAAAAGAA ATTAGTAACC TTGAAATATT 900
ACTTGGAGGG GCTGATNCTG AAGATGATAC TGCTGCTCTT CAAAATAAAT TAGCTACTAA 960
AAAAGCTGAA TTGGAAAAAA CTCAAAAAGA ATTAGATGCA GCTCTTAATG AGTTAGGCCC 1020
TGATGGAGAT GAAGAAGAAA CTCCAGCGCC GGCTCCTCAA CCAGAGCAAC CAGCTCCTGC 1080
ACCAAAACCA GAGCAACCAG CTCCAGCTCC AAAACCAGAG CAACCAGCTC CTGCACCAAA 1140
ACCAGAGCAA CCAGCTCCAG CTCCAAAACC AGAGCAACCA GCTCCAGCTC CAAAACCAGA 1200
GCAACCAGCT AAGCCGGAGA AACCAGCTGA AGAGCCTACT CAACCAGAAA AACCAGCCAC 1260
TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAT TTCTACAATA CTGATGGTTC 1320
AATGGCAATA GGTGGCTCC AAAACAACGG TTCATGGTAC TACCTAAACG CTAACGGCGC 1380
TATGGCAACA GGTGGGTGA AAGATGGAGA TACCTGGTAC TATCTTGAAG CATCAGGTGC 1440
TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ACAGCAATGG 1500
CGCTATGGCG ACAGGCTGGC TCCAATACAA TGGCTCATGG TACTACCTCA ACGCTAATGG 1560
TGATATGGCG ACAGGATGGC TCCAATACAA CGGTTTCATGG TATTACCTCA ACGCTAATGG 1620
TGATATGGCG ACAGGATGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1680
TGCTATGGCT ACAGGTTGGG CTAAAGTCAA CGGTTTCATGG TACTACCTAA ACGCTAACGG 1740
TTCAATGGCA ACAGGTTGGG TGAAAGATGG AGATACCTGG TACTATCTTG AAGCATCAGG 1800
TGCTATGAAA GCAAGCCAAT GGTTCAAAGT ATCAGATAAA TGGTACTATG TCAATGGCTT 1860
AGGTGCCCTT GCAGTCAACA CAACTGTAGA TGGCTATAAA GTCAATGCCA ATGGTGAATG 1920
GGTT 1924

(2) INFORMATION FOR SEQ ID NO:160:

09765272.012001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1           5           10           15

Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
          20           25           30

Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
          35           40           45

Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
          50           55           60

Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65           70           75           80

Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
          85           90           95

Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
          100          105          110

Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
          115          120          125

Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
          130          135          140

Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
145          150          155          160

Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
          165          170          175

Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
          180          185          190

Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
          195          200          205

Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
          210          215          220

Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
225          230          235          240

Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
          245          250          255

Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
          260          265          270

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0965273 013304
 T02210 2229460

Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala
 275 280 285
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala
 290 295 300
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys
 305 310 315 320
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn
 325 330 335
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro
 340 345 350
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro
 355 360 365
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro
 370 375 380
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu
 385 390 395 400
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu
 405 410 415
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp
 420 425 430
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn
 435 440 445
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly
 450 455 460
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala
 465 470 475 480
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val
 485 490 495
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser
 500 505 510
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln
 515 520 525
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr
 530 535 540
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
 545 550 555 560
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu
 565 570 575
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr
 580 585 590
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe
 595 600 605

09765272-012201

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala
 610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp
 625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA 60
 ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAATC GCATTGTAGA 120
 TCCTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT 180
 CTATGGTTAC TTGTCTATTC CAAGTTTGGA AATCATGGAG CCGGTTTATT TGGGAGCAGA 240
 TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG 300
 TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG 360
 CCATTTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCTA CCTTTAATAA 540
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC 600
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu
 1 5 10 15
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu
 20 25 30

Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu
 35 40 45
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu
 50 55 60
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp
 65 70 75 80
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu
 85 90 95
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala
 100 105 110
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly
 115 120 125
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met
 130 135 140
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser
 145 150 155 160
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro
 165 170 175
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr
 180 185 190
 Gln Lys Ser Asp Pro Gln Thr Ala Val Ala Arg Val Ala Phe Thr
 195 200 205
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA	60
TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACTCGCC AATTTAATGC	120
TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCGT AGCCAGGAAG AAACGACCCG	180
TCAGTACCAA CTTCAAGCCC TTTCGAGCCA GATTAATCCA CATTTCTCTT ATAACACTTT	240
GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA	300
GTCCTTGGCA ACCTATTTCC GCTTGGCGCT CAATCAAGGC AAGGACTTGA TTTGTCTCTC	360
TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780
 TAGC 784

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser
 1 5 10 15
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg
 20 25 30
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu
 35 40 45
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu
 50 55 60
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu
 65 70 75 80
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val
 85 90 95
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln
 100 105 110
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln
 115 120 125
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu
 130 135 140
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val
 145 150 155 160
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys
 165 170 175
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly
 180 185 190

Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly
 195 200 205
 Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn
 210 215 220
 Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys
 225 230 235 240
 Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn
 245 250 255
 Arg Ile Glu Thr Ser
 260

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240
GGACAATGTC ATAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile	1 5 10 15
Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His	20 25 30
Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys	35 40 45
Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly	50 55 60

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA	60
TTTGTAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA	120
ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC	180
AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC	238

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln	
1 5 10 15	
Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp	
20 25 30	
His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe	
35 40 45	
Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu	
50 55 60	
Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu	
65 70 75	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

(2) INFORMATION FOR SEQ ID NO:170:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr	Tyr	Gln	Ser	Ser	Ser	Ser	Ala	Ile	Glu	Ala	Thr	Ile	Glu	Gly	Asn
1				5					10					15	
Ser	Gln	Thr	Thr	Ile	Ser	Gln	Thr	Ser	His	Phe	Ile	Gln	Ser	Tyr	Ile
			20					25					30		
Lys	Lys	Leu	Glu	Thr	Thr	Ser	Thr	Gly	Leu	Thr	Gln	Gln	Thr	Asp	Val
		35					40					45			
Leu	Ala	Tyr	Ala	Glu	Asn	Pro	Ser	Gln	Asp	Lys	Val	Glu	Gly	Ile	Arg
	50					55					60				
Asp	Leu	Phe	Leu	Thr	Ile	Leu	Lys	Ser	Asp	Lys	Asp	Leu	Lys	Thr	Val
65					--70--					75					80
Val	Leu	Val	Thr	Lys	Ser	Gly	Gln	Val	Ile	Ser	Thr	Asp	Asp	Ser	Val
				85					90					95	

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys
 100 105 110
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser
 115 120 125
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys
 130 135 140
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu
 145 150 155 160
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe
 165 170 175
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val
 180 185 190
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr
 195 200 205
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys
 210 215 220
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys
 225 230 235 240
 Leu Asp Gln Val Arg Ser Gln
 245

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA 60
 GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTGAGGCCT ATGGTCTTCG 120
 TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA 180
 GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG 240
 TGCTGGTGAG TGGTTCCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA 300
 CCCAGCCTTG ATTATGATTG CAGTGAAGTA AGCACCAGGC CTTGAAATCC ACCTTTCTAC 360
 CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG 420
 TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA 480
 TGTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC 540
 TCTTTCAAAC CACATGAGTA TCGGTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG 600

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCACTA 780
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGAAGGTTG CCCAACGTGA 900
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960
 TCGTAAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTTG CATGATGCTA AAGGCAATAA 1140
 AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260
 AACCAGCGTC ACAGTTCGTG CT 1282

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu
 1 5 10 15
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile
 20 25 30
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe
 35 40 45
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys
 50 55 60
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly
 65 70 75 80
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val
 85 90 95
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro
 100 105 110
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu
 115 120 125
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala
 130 135 140

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp
 145 150 155 160
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser
 165 170 175
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg
 180 185 190
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met
 195 200 205
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu
 210 215 220
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp
 225 230 235 240
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa
 245 250 255
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val
 260 265 270
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp
 275 280 285
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly
 290 295 300
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg
 305 310 315 320
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp
 325 330 335
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu
 340 345 350
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr
 355 360 365
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala
 370 375 380
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln
 385 390 395 400
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr
 405 410 415
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
 420 425

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 778 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA ATCGTCGCGT 60
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360
 CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTTAAACT 420
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile
 1 5 10 15
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys
 20 25 30
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr
 35 40 45
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile
 50 55 60
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg
 65 70 75 80
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu
 85 90 95
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu
 100 105 110

09765273 012301

(2) INFORMATION FOR SEQ ID NO: 175:

(A) LENGTH: 694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGTAAATGCG	CAATCAAATT	CATTAATATT	AATAGATGAA	CCTGAAATCT	CACTTCATCC	60
GAGTGCAATC	TATAAATTTA	AAGAGTTTTT	ACTTCAAGAG	TGTTTAAATA	AAAAACATCA	120
AATTATTATC	ACTACACATT	CTACACAACT	TATAAAAGAT	TTTCCTAGAG	AAGCCGTGAA	180
ACTTTTAGTG	AAAAACGGAG	AAAAGGTAGA	TGTTATTGAA	AATATTGATT	ATCAGGATGC	240
ATTTTTTGAA	TTAGGTGATG	TGTATCATT	TAGGAAGATG	ATTTATGTTG	AAGATAGACT	300
AGCTAAATAT	ATTCTAGAGT	TTGTTATCAC	TCATTCAGGT	AGTGAGAATC	TTAAACAGAA	360
TTTAGTAGTG	AGATATATTC	CTGGTGGAGC	AAATCAAATA	ATTTGTAATA	ATATTTTAAA	420
CTCATCGTAT	TTAGATTCCG	ATAACCATTA	TTTTTGGCTT	GATGGAGATC	AAAACACTAA	480
TGTTAGTGAA	TCAAATAATT	TAATGAACTA	TCTTGAAAAT	GGTGTGTGTA	TATCAGATAA	540
AATTCCTGAA	TCAGATAATA	AAAATCTTGA	TGATATTATA	AAATTGATAA	NGGGATGTCC	600

660

694

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ile Asp Tyr Trp Ala Lys Tyr
225 230

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

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TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT      60
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA      120
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA      180
CACCATCAAT GATAATGCCT CTAGCATTCG GCAAGGCATT CAAACTCTGA CAGGCAATCT      240
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG      300
ACCTGCCTAT ATCGATTTTA TCGCCCCAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA      360
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGAAT AGGACTGGAA AGACTTATAG      420
TTATATTCAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAACTA      480
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC      540
AACATCTGGC                                     550

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(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met
1           5           10           15
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu
20        25        30
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val
35        40        45
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp
50        55        60
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu
65        70        75        80
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala
85        90        95
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

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284

100	105	110
Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala		
115	120	125
Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro		
130	135	140
Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr		
145	150	155
Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe		
165	170	175
Thr Leu Phe Ser Thr Ser Gly		
180		

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA	60
GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTTG CGCGACCCAG CAGAATTCCA	120
CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC	180
AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC	240
AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG	300
CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC	334

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val	
1	15
Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp	
20	30
Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg	
35	45

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys
50 55 60

Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr
65 70 75 80

Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile
85 90 95

Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAACTT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGTTTATGTC TTAAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAAGT GGTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCAAACAAT AGTCTAGCAA CACCTTCTCC	1200

(2) INFORMATION FOR SEQ ID NO:182:

(A) LENGTH: 447 amino acids

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro
20 25 30

Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile
35 40 45

Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His
50 55 60

Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu
65 70 75 80

Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn
85 90 95

Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val
100 105 110

Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu
115 120 125

Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn
130 135 140

Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp
145 150 155 160

Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala
165 170 175

Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp
180 185 190

Leu Ser Ala Ser Glu Leu Ala Ala Lys Ala His Leu Ala Gly Lys
195 200 205

Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn
210 215 220

Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

(2) INFORMATION FOR SEQ ID NO: 183:

(A) LENGTH: 934 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGACTACCTT	GAAATCCCAC	TTTACAGCTA	TCTTGGTGGA	TTCAACACTA	AAGTTCTTCC	60
AACTCCAATG	ATGAACATCA	TCAACGGTGG	TTCTCACTCT	GACGCTCCAA	TCGCTTTCCA	120
AGAGTTCATG	ATCTTGCCAG	TTGGTGCGCC	AACATTTAAA	GAAGCCCTTC	GTTACGGTGC	180
TGAAATCTTC	CACGCTCTTA	AGAAAATCCT	TAAATCACGT	GGTTTGGA	CTGCCGTAGG	240
TGACGAAGGT	GGATTCGCTC	CTCGTTTCGA	AGGAACTGAA	GATGGTGTTG	AAACTATCCT	300

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420
 TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGTTGGAA 540
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660
 AGTTAACCAA ATCGGTACTC TTAAGTAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp	Tyr	Leu	Glu	Ile	Pro	Leu	Tyr	Ser	Tyr	Leu	Gly	Gly	Phe	Asn	Thr	1	5	10	15
Lys	Val	Leu	Pro	Thr	Pro	Met	Met	Asn	Ile	Ile	Asn	Gly	Gly	Ser	His	20	25	30	
Ser	Asp	Ala	Pro	Ile	Ala	Phe	Gln	Glu	Phe	Met	Ile	Leu	Pro	Val	Gly	35	40	45	
Ala	Pro	Thr	Phe	Lys	Glu	Ala	Leu	Arg	Tyr	Gly	Ala	Glu	Ile	Phe	His	50	55	60	
Ala	Leu	Lys	Lys	Ile	Leu	Lys	Ser	Arg	Gly	Leu	Glu	Thr	Ala	Val	Gly	65	70	75	80
Asp	Glu	Gly	Gly	Phe	Ala	Pro	Arg	Phe	Glu	Gly	Thr	Glu	Asp	Gly	Val	85	90	95	
Glu	Thr	Ile	Leu	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Tyr	Val	Pro	Gly	Lys	100	105	110	
Asp	Val	Phe	Ile	Gly	Phe	Asp	Cys	Ala	Ser	Ser	Glu	Phe	Tyr	Asp	Lys	115	120	125	
Glu	Arg	Lys	Val	Tyr	Asp	Tyr	Thr	Lys	Phe	Glu	Gly	Glu	Gly	Ala	Ala	130	135	140	
Val	Arg	Thr	Ser	Ala	Glu	Gln	Ile	Asp	Tyr	Leu	Glu	Glu	Leu	Val	Asn				

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(2) INFORMATION FOR SEQ ID NO: 185:

(A) LENGTH: 541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCGTATCTTT	TTTTGGAGCA	ATGTTGCGGT	AGAAGGACAT	TCCATGGATC	CGACCCTAGC	60
GGATGGCGAA	ATTCTCTTCG	TTGTAAAAACA	CCTTCCTATT	GACCGTTTTG	ATATCGTGGT	120
GGCCCCATGAG	GAAGATGGCA	ATAAGGACAT	CGTCAAGCGC	GTGATTGGAA	TGCCTGGCGA	180
CACCATTTCGT	TACGAAAATG	ATAAACTCTA	CATCAATGAC	AAAGAAACGG	ACGAGCCTTA	240
TCTAGCAGAC	TATATCAAAC	GCTTCAAGGA	TGACAAACTC	CAAAGCACTT	ACTCAGGCAA	300
GGGCTTTGAA	GGAAATAAAG	GAACTTTCTT	TAGAAGTATC	GCTCAAAAAG	CTCAAGCCTT	360
CACAGTTGAT	GTCAACTACA	ACACCAACTT	TAGCTTTACT	GTTCCAGAAG	GAGAATACCT	420
TCTCCTCGGA	GATGACCGCT	TGGTTTCGAG	CGACAGCCGC	CACGTAGGTA	CCTTCAAAGC	480
AAAAGATATC	ACAGGGGAAG	CTAAATTCCG	CTTATGGCCA	ATCACCCGTA	TCGGAACATT	540
T						541

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp
1 5 10 15

Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro
20 25 30

Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys
35 40 45

Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr
50 55 60

Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr
65 70 75 80

Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr
85 90 95

Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser
100 105 110

Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr
115 120 125

Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp
130 135 140

Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala
145 150 155 160

Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg
165 170 175

Ile Gly Thr Phe
180

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180
 GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAGTC CTTGCCAAAG CCCAAACCT 300
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala
 1 5 10 15
 Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser
 20 25 30
 Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val
 35 40 45
 Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg
 50 55 60
 Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val
 65 70 75 80
 Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys
 85 90 95
 Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn
 100 105 110
 Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile
 115 120 125
 Leu Asp Lys Leu Lys
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CTCTCAGGC TATTCTCAGT CAGCCATCTT 180
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300
 GACTTTTTTG AACTATGTTT AGCAATACAC CAAGCCCTTT AACGATATTT CTTCACTGCT 360
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAATAATC 600
 AACTCTTATC AATCTCCTTA TGCCTTTTTC TCCATTAGC TCGGGAGATA TCTTGCTGGA 660
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCAG CCATTTCAGGA 1080
 TGCGGATTTA ATTCTTGTCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200
 A 1201

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile
 1 5 10 15
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln
 20 25 30

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Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His
 35 40 45
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr
 50 55 60
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu
 65 70 75 80
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val
 85 90 95
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro
 100 105 110
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala
 115 120 125
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu
 130 135 140
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile
 145 150 155 160
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile
 165 170 175
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val
 180 185 190
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg
 195 200 205
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile
 210 215 220
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu
 225 230 235 240
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe
 245 250 255
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala
 260 265 270
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr
 275 280 285
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu
 290 295 300
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu
 305 310 315 320
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln
 325 330 335
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala
 340 345 350
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val
 355 360 365

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Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG	60
AAAAGCAGTG AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC	120
TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC	180
CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC	240
AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT	300
CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAACAAG GAAATGATGT	360
GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA	420
CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA	480
CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA	540
TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA	600
TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC	660
CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG	720
TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAAGACA AATTTGAGTC	780
TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA	840
AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT	900
TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG	960
CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT	1020
AGATTATGTT GAT	1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg	Asn	Ala	Gly	Gln	Thr	Asp	Ala	Ser	Gln	Ile	Glu	Lys	Ala	Ala	Val	1	5	10	15
Ser	Gln	Gly	Gly	Lys	Ala	Val	Lys	Lys	Thr	Glu	Ile	Ser	Lys	Asp	Ala	20	25	30	
Asp	Leu	His	Glu	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu	35	40	45	
Glu	Tyr	Phe	Ser	Arg	Val	Pro	Gly	Val	Thr	Asp	Ala	Val	Ser	Gly	Tyr	50	55	60	
Ala	Asn	Gly	Arg	Gly	Glu	Thr	Thr	Lys	Tyr	Glu	Leu	Ile	Asn	Gln	Thr	65	70	75	80
Gly	His	Ala	Glu	Thr	Val	His	Val	Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser	85	90	95	
Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser	100	105	110	
Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val	115	120	125	
Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	Glu	Val	Ile	Asn	Gln	Val	Phe	Asp	130	135	140	
Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn	145	150	155	160
Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	165	170	175	
Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr	180	185	190	
Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu	195	200	205	
Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln	210	215	220	
Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly	225	230	235	240
Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	245	250	255	
Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser	260	265	270	
Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg	275	280	285	
Met	Glu	Val	Arg	Ser	Arg	Val	Gly	Asp	Ser	His	Leu	Gly	His	Val	Phe	290	295	300	
Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	305	310	315	320

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Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT TTAGCGCTTG TTCTTCTAAT TCTGNTAAAA ATGAAGAAAA TACTTCTAAA	60
GAGCATGCGC CTGATAAAAT AGTTTTAGAT CATGCTTTTCG GTCAAACATAT ATTAGATAAA	120
AAACCTGAAA GAGTTGCAAC TATTGCTTGG GGAAATCATG ATGTAGCATT AGCTTTAGGA	180
ATAGTTCCTG TTGGATTTTC AAAAGCAAAT TACGGTGTA GTGCTGATAA AGGAGTTTTA	240
CCATGGACAG AAGAAAAAAT CAAAGAACTA AATGGTAAAG CTAACCTATT TGACGATTTG	300
GATGGACTTA ACTTTGAAGC AATATCAAAT TCTAAACCAG ATGTTATCTT AGCAGGTTAT	360
TCTGGTATAA CTAAAGAAGA TTATGACACT CTATCA	396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys Ile Val Phe Ser Ala Cys Ser Ser Asn Ser Xaa Lys Asn Glu Glu	
1 5 10 15	
Asn Thr Ser Lys Glu His Ala Pro Asp Lys Ile Val Leu Asp His Ala	
20 25 30	
Phe Gly Gln Thr Ile Leu Asp Lys Lys Pro Glu Arg Val Ala Thr Ile	
35 40 45	
Ala Trp Gly Asn His Asp Val Ala Leu Ala Leu Gly Ile Val Pro Val	
50 55 60	
Gly Phe Ser Lys Ala Asn Tyr Gly Val Ser Ala Asp Lys Gly Val Leu	
65 70 75 80	
Pro Trp Thr Glu Glu Lys Ile Lys Glu Leu Asn Gly Lys Ala Asn Leu	
85 90 95	

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Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys
 100 105 110

Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr
 115 120 125

Asp Thr Leu Ser
 130

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAATATA GAAATTATTT TAGTTGATGA	60
CGGTTCTACG GATAATTCTG GGGAAATTTG TGATGCTTTT ATGATGCAAG ATAATCGTGT	120
GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG	180
TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTTCAGAT GATATCGTAA AAGAAAATAT	240
GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA	300
CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTAACAGGGC AAGATTTTTG	360
CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA	420
TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT	480
TCACTTTTCA AATGGTCGCC GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT	540
AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG	600
CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTTCTAA	660
GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT	720
CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTAACAG ATACTGAGGA	780
ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA	840
AAGT	844

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09765272 012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile
 1 5 10 15
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala
 20 25 30
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys
 35 40 45
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly
 50 55 60
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met
 65 70 75 80
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val
 85 90 95
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe
 100 105 110
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu
 115 120 125
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe
 130 135 140
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val
 145 150 155 160
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg
 165 170 175
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr
 180 185 190
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu
 195 200 205
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp
 210 215 220
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val
 225 230 235 240
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr
 245 250 255
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe
 260 265 270
 Asp Ala Glu Gln Arg Asn Gly Lys Ser
 275 280

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA 60
TGGCTCTCCA GATCATTTCAT CCAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120
CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180
TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240
AGACCGATTA TATGGTGCTT TGAAAAGGA AAACGCAGAT ATTAGTATCG GGC GTTATAA 300
TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360
AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420
GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480
TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540
GAGGATAGTC TATTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600
ATCGAATACA TGGAGTGAAG AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660
AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720
ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTCACAG 780
AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu
1 5 10 15
Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu
20 25 30
Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly
35 40 45
Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala
50 55 60
Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu
65 70 75 80
Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile
85 90 95

09765972 012204

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr
 100 105 110
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile
 115 120 125
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val
 130 135 140
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe
 145 150 155 160
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu
 165 170 175
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr
 180 185 190
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg
 195 200 205
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala
 210 215 220
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg
 225 230 235 240
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr
 245 250 255
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA 60
 TGCTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT 120
 TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA 180
 TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT 240
 AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA 300
 TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA 360
 GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGTAT GAAACTCAAG AAATGAAGAG 420
 TTTTGCTTTG ATATCTGCTT GGGGTAAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG 480
 CTTTGACATA GGTAAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC 540

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840
 GAAAGCCATT GTCCTCGCAG CAAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900
 GTCTATTTGT TATCATAATC GTTCGATTCTG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260
 TCTCTGGTA AACAATGCTT TTTGGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320
 AACCAATGAA TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500
 TCGGAAACCG TGGAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTAAAGATAG CAGCTAGAGT 1740
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800
 AATTCATCTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860
 TATTAATCAT GGCGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920
 TATCTTATCC TTTGAAAATA CTAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val
 1 5 10 15
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu
 20 25 30
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala
 35 40 45
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn
 50 55 60
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val
 65 70 75 80
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val
 85 90 95
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His
 100 105 110
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile
 115 120 125
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile
 130 135 140
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg
 145 150 155 160
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val
 165 170 175
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala
 180 185 190
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp
 195 200 205
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala
 210 215 220
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met
 225 230 235 240
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr
 245 250 255
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu
 260 265 270
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn
 275 280 285
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr
 290 295 300
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn
 305 310 315 320
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu
 325 330 335

00765373 012304

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln Ile Ser Cys Tyr Lys Ser
 340 345 350
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val
 355 360 365
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys
 370 375 380
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala
 385 390 395 400
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe
 405 410 415
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn
 420 425 430
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val
 435 440 445
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp
 450 455 460
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe
 465 470 475 480
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His
 485 490 495
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr
 500 505 510
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly
 515 520 525
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile
 530 535 540
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu
 545 550 555 560
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile
 565 570 575
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr
 580 585 590
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp
 595 600 605
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly
 610 615 620
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro
 625 630 635 640
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala
 645 650 655
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile
 660 665 670

056522 012201
 102210 2259460

Ser Lys

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTCAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA	60
TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA	120
TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG ATGAAGCAGG CTCACGGGGA	180
TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA	240
TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC	300
TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC	360
ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT	420
CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA	480
TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCTATTA	540
TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC	600
CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA	660
AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT	720
AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAGGCCA	780
TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC	840
CCTATTCATA AATATTTCTT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA	900
AAAATTACAT	910

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile	Gln	Lys	Gln	Thr	Tyr	Gln	Asn	Leu	Glu	Ile	Ile	Leu	Val	Asp	Asp
1				5				10						15	

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln
 20 25 30
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln
 35 40 45
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe
 50 55 60
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr
 65 70 75 80
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met
 85 90 95
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp
 100 105 110
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly
 115 120 125
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile
 130 135 140
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr
 145 150 155 160
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr
 165 170 175
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys
 180 185 190
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe
 195 200 205
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe
 210 215 220
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu
 225 230 235 240
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe
 245 250 255
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys
 260 265 270
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr
 275 280 285
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
 290 295 300

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTC AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT	60
TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG	120
AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC	180
AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA	240
TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC	300
GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG	360
TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC	420
GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA	480
TCATGAAAAA TGGTCTCGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA	540
AAAATATCAT AAAAATTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG	600
TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC	660
AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC	720
TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA	780
TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC	840
AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCTTTA GACATGCTAT	900
ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAATAGA ACAAAGCTG TATTTTGGAA	960
TGGAGAAGGT AGGATTAGTT CATTAACGG ATTTTATCAA GGACTTTATT CGAATGATGA	1020
AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT	1080
TGATAAGGAA AAGATTTTAT CTATATTCCC TAATGCAAAA ATTTTGACTA AAAATAGTGA	1140
GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA	1200
TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA	1260
TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA	1320
TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTTAC ATATTTTATT	1380
GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC	1440
AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT	1500
CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAAGGGC ATACTGGTCA	1560
TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA	1620
TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT	1680
AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA	1740
TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC	1800

(2) INFORMATION FOR SEQ ID NO:204:

(A) LENGTH: 657 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys	Ala	Asp	Asn	Arg	Val	Gln	Met	Arg	Thr	Ile	Asn	Asn	Glu	Ser	
1			5						10				15		
Pro	Leu	Leu	Leu	Ser	Pro	Leu	Tyr	Gly	Asn	Asp	Asn	Gly	Asn	Gly	Leu
			20					25					30		
Trp	Trp	Gly	Asn	Thr	Leu	Lys	Gly	Ala	Trp	Glu	Ala	Ile	Pro	Glu	Asp
		35					40					45			
Val	Lys	Pro	Tyr	Ala	Ala	Ile	Glu	Leu	His	Pro	Ala	Lys	Val	Cys	Lys
	50					55					60				
Pro	Thr	Ser	Cys	Ile	Pro	Arg	Asp	Thr	Lys	Glu	Leu	Arg	Glu	Trp	Tyr
65					70					75					80
Val	Lys	Met	Leu	Glu	Glu	Ala	Gln	Ser	Leu	Asn	Ile	Pro	Val	Phe	Leu
				85					90					95	
Val	Ile	Met	Ser	Ala	Gly	Glu	Arg	Asn	Thr	Val	Pro	Pro	Glu	Trp	Leu
			100					105					110		
Asp	Glu	Gln	Phe	Gln	Lys	Tyr	Ser	Val	Leu	Lys	Gly	Val	Leu	Asn	Ile
		115					120					125			
Glu	Asn	Tyr	Trp	Ile	Tyr	Asn	Asn	Gln	Leu	Ala	Pro	His	Ser	Ala	Lys
	130					135					140				
Tyr	Leu	Glu	Val	Cys	Ala	Lys	Tyr	Gly	Ala	His	Phe	Ile	Trp	His	Asp
145					150					155					160
His	Glu	Lys	Trp	Phe	Trp	Glu	Thr	Ile	Met	Asn	Asp	Pro	Thr	Phe	Phe
				165					170					175	
Glu	Ala	Ser	Gln	Lys	Tyr	His	Lys	Asn	Leu	Val	Leu	Ala	Thr	Lys	Asn
			180					185					190		
Thr	Pro	Ile	Arg	Asp	Asp	Ala	Gly	Thr	Asp	Ser	Ile	Val	Ser	Gly	Phe
		195					200					205			
Trp	Leu	Ser	Gly	Leu	Cys	Asp	Asn	Trp	Gly	Ser	Ser	Thr	Asp	Thr	Trp
	210					215					220				
Lys	Trp	Trp	Glu	Lys	His	Tyr	Thr	Asn	Thr	Phe	Glu	Thr	Gly	Arg	Ala

225 230 235 240
 Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met
 245 250 255
 Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu
 260 265 270
 Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe
 275 280 285
 Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala
 290 295 300
 Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn
 305 310 315 320
 Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr
 325 330 335
 Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile
 340 345 350
 Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile
 355 360 365
 Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser
 370 375 380
 Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp
 385 390 395 400
 Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn
 405 410 415
 Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn
 420 425 430
 Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val
 435 440 445
 Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg
 450 455 460
 Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser
 465 470 475 480
 Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys
 485 490 495
 Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu
 500 505 510
 Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly
 515 520 525
 Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His
 530 535 540
 Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile
 545 550 555 560
 Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe

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565 570 575

Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser
580 585 590

Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg
595 600 605

Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn
610 615 620

Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu
625 630 635 640

Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn
645 650 655

Phe

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTTC	60
ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG	780
TGGCAAATTA ACCACCTGGG ACAAGATTAA A	811

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	
1				5				10					15			
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	
			20				25						30			
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	
		35				40						45				
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	
		50				55					60					
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	
65				70					75					80		
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	
			85					90					95			
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	
			100					105					110			
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	
		115				120						125				
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	
		130				135					140					
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	
145					150					155				160		
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	
			165					170					175			
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	
		180						185					190			
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	
		195					200					205				
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	
		210				215					220					
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	
225				230						235				240		
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	
			245					250					255			
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys			
			260					265					270			

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTGAT GCATTTTTTA ATCTCGTTAA 180
 TGACTATAAT ACCATTGTCT GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA 240
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360
 GCTTGAAAAG AATGACCACT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480
 AACTACAGAT GTCAAGGTTT ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GCTTTCTTAT TTGTAGAGAA 660
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780
 GGATAATGAT AAGTGGGTTA AACTT 805

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser
 1 5 10 15
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn
 20 25 30
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp
 35 40 45
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr
 50 55 60

Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His
 65 70 75 80
 Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys
 85 90 95
 Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu
 100 105 110
 Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu
 115 120 125
 Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln
 130 135 140
 Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser
 145 150 155 160
 Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser
 165 170 175
 Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His
 180 185 190
 Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu
 195 200 205
 Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu
 210 215 220
 Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys
 225 230 235 240
 Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys
 245 250 255
 Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu
 260 265

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCT TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCCAGTCCT	360

AGTTGACCCA TCAGGCAAAC TTTTGGAAAC TTATGGTGTG CGTTCTTACC CAACCCAAGC 420
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys	Ser	Gly	Lys	Ser	Val	Thr	Ser	Glu	His	Gln	Thr	Lys	Asp	Glu	Met
1			5						10					15	
Lys	Thr	Glu	Gln	Thr	Ala	Ser	Lys	Thr	Ser	Ala	Ala	Lys	Gly	Lys	Glu
		20						25					30		
Val	Ala	Asp	Phe	Glu	Leu	Met	Gly	Val	Asp	Gly	Lys	Thr	Tyr	Arg	Leu
		35					40					45			
Ser	Asp	Tyr	Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp
	50					55					60				
Cys	Ser	Ile	Cys	Leu	Ala	Ser	Leu	Pro	Asp	Thr	Asp	Glu	Ile	Ala	Lys
65				70						75					80
Glu	Ala	Gly	Asp	Asp	Tyr	Val	Val	Leu	Thr	Val	Val	Ser	Pro	Gly	His
			85						90					95	
Lys	Gly	Glu	Gln	Ser	Glu	Ala	Asp	Phe	Lys	Asn	Trp	Tyr	Lys	Gly	Leu
			100					105						110	
Asp	Tyr	Lys	Asn	Leu	Pro	Val	Leu	Val	Asp	Pro	Ser	Gly	Lys	Leu	Leu
		115					120					125			
Glu	Thr	Tyr	Gly	Val	Arg	Ser	Tyr	Pro	Thr	Gln	Ala	Phe	Ile	Asp	Lys
		130				135					140				
Glu	Gly	Lys	Leu	Val	Lys	Thr	His	Pro	Gly	Phe	Met	Glu	Lys	Asp	Ala
145					150					155					160
Ile	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Ala							
				165											

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

09765272.012201

CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60
TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTCT GGGGAGTGGA 120
GGAATATTTC TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180
AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240
CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300
CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360
TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420
GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480
GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540
TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600
GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660
TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720
GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTTAC 780
CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840
TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTGGG CATGTCTTTA CGGATGGTCC 900
ACAGGACAAG GGCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960
AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser Gln Ile Glu Lys Ala Ala Val Ser Gln Gly Gly Lys Ala Val Lys
1 5 10 15
Lys Thr Glu Ile Ser Lys Asp Ala Asp Leu His Glu Ile Tyr Leu Ala
20 25 30
Gly Gly Cys Phe Trp Gly Val Glu Glu Tyr Phe Ser Arg Val Pro Gly
35 40 45
Val Thr Asp Ala Val Ser Gly Tyr Ala Asn Gly Arg Gly Glu Thr Thr
50 55 60
Lys Tyr Glu Leu Ile Asn Gln Thr Gly His Ala Glu Thr Val His Val
65 70 75 80

315

Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser	Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	
				85					90					95		
Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser	Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	
			100					105					110			
Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val	Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	
		115					120					125				
Glu	Val	Ile	Asn	Gln	Val	Phe	Asp	Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	
	130					135					140					
Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn	Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	
145					150					155					160	
Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	
			165						170					175		
Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr	Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	
			180					185					190			
Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu	Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	
		195					200					205				
Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln	Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	
	210					215					220					
Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly	Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	
225					230					235				240		
Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	
			245						250				255			
Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser	Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	
			260					265					270			
Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg	Met	Glu	Val	Arg	Ser	Arg	Val	Gly	
	275					280					285					
Asp	Ser	His	Leu	Gly	His	Val	Phe	Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	
	290					295					300					
Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Leu	Ser	Ile	Arg	Phe	Ile	Pro	Lys	
305					310					315				320		
Asp	Gln	Met	Glu	Glu	Lys	Gly	Thr	Leu	Ile	Tyr						
			325					330								

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA	GGTTCTAATG	GTTCTCAGTC	TGCTGTGGAT	GCTATCAAAC	AAAAAGGGAA	60
ATTAGTTGTG	GCAACCAGTC	CTGACTATGC	ACCCTTTGAA	TTTCAATCAT	TGGTTGATGG	120

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180
 GGTAAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAAGTGG 240
 TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300
 TTTTTCATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360
 AAAATACAAG GATTTAAC TA GCCTAGAAAG TGCTAATATT GCAGCCCAA AAGGGACTGT 420
 TCCAGAAATCA ATGGTCAAGG AACAAATGCC AAAAGTTCAA TTAAGTTCCC TAACTAATAT 480
 GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTCATA TGGATGAGCC 540
 TGTGCACTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600
 GATGAAGGAC GGCGACGCCA ATGCC 625

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys	Gln	Ser	Gly	Ser	Asn	Gly	Ser	Gln	Ser	Ala	Val	Asp	Ala	Ile	Lys	1	5	10	15
Gln	Lys	Gly	Lys	Leu	Val	Val	Ala	Thr	Ser	Pro	Asp	Tyr	Ala	Pro	Phe	20	25	30	
Glu	Phe	Gln	Ser	Leu	Val	Asp	Gly	Lys	Asn	Gln	Val	Val	Gly	Ala	Asp	35	40	45	
Ile	Asp	Met	Ala	Gln	Ala	Ile	Ala	Asp	Glu	Leu	Gly	Val	Lys	Leu	Glu	50	55	60	
Ile	Ser	Ser	Met	Ser	Phe	Asp	Asn	Val	Leu	Thr	Ser	Leu	Gln	Thr	Gly	65	70	75	80
Lys	Ala	Asp	Leu	Ala	Val	Ala	Gly	Ile	Ser	Ala	Thr	Asp	Glu	Arg	Lys	85	90	95	
Glu	Val	Phe	Asp	Phe	Ser	Ile	Pro	Tyr	Tyr	Glu	Asn	Lys	Ile	Ser	Phe	100	105	110	
Leu	Val	Arg	Lys	Ala	Asp	Val	Glu	Lys	Tyr	Lys	Asp	Leu	Thr	Ser	Leu	115	120	125	
Glu	Ser	Ala	Asn	Ile	Ala	Ala	Gln	Lys	Gly	Thr	Val	Pro	Glu	Ser	Met	130	135	140	
Val	Lys	Glu	Gln	Leu	Pro	Lys	Val	Gln	Leu	Thr	Ser	Leu	Thr	Asn	Met	145	150	155	160
Gly	Glu	Ala	Val	Asn	Glu	Leu	Gln	Ala	Gly	Lys	Ile	Asp	Ala	Val	His				

09163332 012201
 102210 222546

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT 60
 TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA 120
 AAATTCCAAT AAATCCCAAG GAGATTATAC GGAATCATTG GTGAATAAAA ACACAGAAAA 180
 TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA 240
 AAAAGCAATC AAGGAACTAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG 300
 AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT 360
 AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG 420
 AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG 480
 GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG 540
 ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA 600
 CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA 660
 TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC 720
 ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA 780
 CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTG 840
 TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT 900
 CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGATAG 960
 TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC 1020
 TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA 1080
 TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC 1140
 GGTGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG 1200
 TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA 1260
 TGGAACAAAA GCTCCTAGTA AATTAAATTT TGTATATATA GGCAAGGGGC AAGACCAAGA 1320

05652 012201
 102210 225946

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500
 GGATGAAGGT ACTAAAAGTC AAGTGT'TTC AAT'TTCAGGA GATGATGGTG TAAAGCTATG 1560
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620
 AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800
 TTTAAAACCC GATGTTTCAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAACCTCA TATGGTTCCA TTTCTCTTAA 2220
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATG TTCCAGAAAT 2400
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTGATG CCTCTAATGG GATTTGCTGG 2640
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700
 AACACTGGGA GGTTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAAG 3000
 AAGTGCAGAA GAAGGATTGA TT 3022

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

09765273 012301

(ii) MOLECULE TYPE: protein

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu
1				5					10					15	
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn
			20					25					30		
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp
		35					40					45			
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu
	50					55					60				
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu
65				70						75					80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr
				85					90					95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp
			100					105					110		
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg
		115					120					125			
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly
	130					135					140				
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly
145					150					155					160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly
				165					170					175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala
			180					185					190		
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr
		195					200					205			
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly
	210					215					220				
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro
225					230					235					240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln
				245					250					255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln
			260					265					270		
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly
		275					280					285			

Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val
 290 295 300
 Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly
 305 310 315 320
 Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro
 325 330 335
 Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser Ser
 340 345 350
 Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn
 355 360 365
 Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala
 370 375 380
 Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser
 385 390 395 400
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr
 405 410 415
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr
 420 425 430
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly
 435 440 445
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala
 450 455 460
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn
 465 470 475 480
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met
 485 490 495
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser
 500 505 510
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys
 515 520 525
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu
 530 535 540
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn
 545 550 555 560
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp
 565 570 575
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser
 580 585 590
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro
 595 600 605
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr
 610 615 620

Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr Pro Ile Val Ala Ala
 625 630 635 640
 Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu Met Leu Glu Arg Pro
 645 650 655
 Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu
 660 665 670
 Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro Met Met Asp Ala Thr
 675 680 685
 Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly
 690 695 700
 Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg Asn Glu Val Val Ala
 705 710 715 720
 Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser
 725 730 735
 Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys
 740 745 750
 Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe Lys Val Ser Ala Ser
 755 760 765
 Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr
 770 775 780
 Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln Ile Val Pro Glu Ile
 785 790 795 800
 His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr Phe Glu His Asp Thr
 805 810 815
 Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu Asn Ala Val Ile Asn
 820 825 830
 Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val Glu Ser Phe Ile His
 835 840 845
 Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn Ser Ser Gly Lys Lys
 850 855 860
 Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu Met Gly Phe Ala Gly
 865 870 875 880
 Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly
 885 890 895
 Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys
 900 905 910
 Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly Glu His Gly Ile Asp
 915 920 925
 Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg Lys Asp Lys Asn Thr
 930 935 940
 Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly
 945 950 955 960

09553 01304

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile
995 1000 1005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA	GTTGAGACTC	CTCAATCAAT	AACAAATCAG	GAGCAAAGCTA	GGACAGAAAA	60
CCAAGTAGTA	GAGACAGAGG	AAGCTCCAAA	AGAAGAAGCA	CCTAAAACAG	AAGAAAGTCC	120
AAAGGAAGAA	CCAAAATCGG	AGGTAAAACC	TACTGACGAC	ACCC'TTCCTA	AAGTAGAAGA	180
GGGGAAAGAA	GATTTCAGCAG	AACCAGCTCC	AGTTGAAGAA	GTAGGTGGAG	AAGTTGAGTC	240
AAAACCAGAG	GAAAAAGTAG	CAGTTAAGCC	AGAAAGTCAA	CCATCAGACA	AACCAGCTGA	300
GGAATCAAAA	GTTGAACAAG	CAGGTGAACC	AGTCGCGCCA	AGAGAAGACG	AAAAGGCACC	360
AGTCGAGCCA	GAAAAGCAAC	CAGAAGCTCC	TGAAGAAGAG	AAGGCTGTAG	AGGAAACACC	420
GAAACAAGAA	GAGTCAACTC	CAGATACCAA	GGCTGAAGAA	ACTGTAGAAC	CAAAAGAGGA	480
GA CTGTTAAT	CAATCTATTG	AACAACCAAA	AGTTGAAACG	CCTGCTGTAG	AAAAACAAAC	540
AGAACCAACA	GAGGAACCAA	AAGTTGAACA	AGCAGGTGAA	CCAGTCGCGC	CAAGAGAAGA	600
CGAACAGGCA	CCAACGGCAC	CAGTTGAGCC	AGAAAAGCAA	CCAGAAGTTC	CTGAAGAAGA	660
GAAGGCTGTA	GAGGAAACAC	CGAAACCAGA	AGATAAAATA	AAGGGTATTG	GTACTAAAGA	720
ACCAGTTGAT	AAAAGTGAGT	TAAATAATCA	AATTGATAAA	GCTAGTTCAG	TTTCTCCTAC	780
TGATTATTCT	ACAGCAAGTT	ACAATGCTCT	TGGACCTGTT	TTAGAAACTG	CAAAAGGTGT	840
CTATGCTTCA	GAGCCTGTAA	AACAGCCTGA	GGTAAATAGC	GAGACAAATA	AACTTAAAAC	900
GGCTATTGAC	GCTCTAAACG	TTGATAAAAC	TGAATTAAAC	AATACGATTG	CAGATGCAAA	960
AACAAAGGTA	AAAGAACATT	ACAGTGATAG	AAGTTGGCAA	AACCTCCAAA	CTGAAGTTAC	1020
AAAGGCTGAA	AAAGTTGCAG	CTAATACAGA	TGCTAAACAA	AGTGAAGTTA	ACGAAGCTGT	1080
TGAAAAATTA	ACTGCAACTA	TTGAAAAATT	GGTTGAATTA	TCTGAAAAGC	CAATATTAAC	1140
ATTGACTAGT	ACCGATAAGA	AAATATTGGA	ACGTGAAGCT	GTTGCTAAGT	ATACTCTAGA	1200
AAATCAAAAC	AAAACAAAAA	TCAAATCAAT	CACAGCTGAA	TTGAAAAAAG	GAGAAGAAGT	1260

TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAACTATAA GCGCTGCATT 1320
 TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380
 TAACGGTGAA GAAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT 1440
 TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAACTAA 1500
 TGAATCACTG ATAACAATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC 1560
 AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAACTA CGGTTAACGG 1620
 AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680
 TAAATTTGAA GAAGAA 1696

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala
 1 5 10 15
 Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu
 20 25 30
 Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val
 35 40 45
 Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp
 50 55 60
 Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser
 65 70 75 80
 Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp
 85 90 95
 Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala
 100 105 110
 Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu
 115 120 125
 Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu
 130 135 140
 Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu
 145 150 155 160
 Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val
 165 170 175
 Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly

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324

180

185

190

Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro	Val
		195					200					205			
Glu	Pro	Glu	Lys	Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu
		210				215					220				
Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu
225					230					235					240
Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser
				245					250					255	
Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	Ala	Ser	Tyr	Asn	Ala	Leu	Gly	Pro
			260					265					270		
Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	Tyr	Ala	Ser	Glu	Pro	Val	Lys	Gln
		275					280					285			
Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	Lys	Leu	Lys	Thr	Ala	Ile	Asp	Ala
		290				295					300				
Leu	Asn	Val	Asp	Lys	Thr	Glu	Leu	Asn	Asn	Thr	Ile	Ala	Asp	Ala	Lys
305					310					315					320
Thr	Lys	Val	Lys	Glu	His	Tyr	Ser	Asp	Arg	Ser	Trp	Gln	Asn	Leu	Gln
				325					330					335	
Thr	Glu	Val	Thr	Lys	Ala	Glu	Lys	Val	Ala	Ala	Asn	Thr	Asp	Ala	Lys
			340					345					350		
Gln	Ser	Glu	Val	Asn	Glu	Ala	Val	Glu	Lys	Leu	Thr	Ala	Thr	Ile	Glu
		355					360					365			
Lys	Leu	Val	Glu	Leu	Ser	Glu	Lys	Pro	Ile	Leu	Thr	Leu	Thr	Ser	Thr
		370				375					380				
Asp	Lys	Lys	Ile	Leu	Glu	Arg	Glu	Ala	Val	Ala	Lys	Tyr	Thr	Leu	Glu
385					390					395					400
Asn	Gln	Asn	Lys	Thr	Lys	Ile	Lys	Ser	Ile	Thr	Ala	Glu	Leu	Lys	Lys
				405					410					415	
Gly	Glu	Glu	Val	Ile	Asn	Thr	Val	Val	Leu	Thr	Asp	Asp	Lys	Val	Thr
			420					425					430		
Thr	Glu	Thr	Ile	Ser	Ala	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys	Glu
		435					440					445			
Tyr	Thr	Leu	Ser	Thr	Thr	Met	Ile	Tyr	Asp	Arg	Gly	Asn	Gly	Glu	Glu
		450				455					460				
Thr	Glu	Thr	Leu	Glu	Asn	Gln	Asn	Ile	Gln	Leu	Asp	Leu	Lys	Lys	Val
465					470					475					480
Glu	Leu	Lys	Asn	Ile	Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Asn	Gly
				485					490					495	
Lys	Glu	Thr	Asn	Glu	Ser	Leu	Ile	Thr	Thr	Ile	Pro	Asp	Asp	Lys	Ser
			500					505					510		
Asn	Tyr	Tyr	Leu	Lys	Ile	Thr	Ser	Asn	Asn	Gln	Lys	Thr	Thr	Leu	Leu

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515 520 525
 Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn Gly Thr Pro Val Tyr
 530 535 540
 Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser Arg Thr Ala Asp Asn
 545 550 555 560
 Lys Phe Glu Glu Glu
 565

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA	60
TAAATTTGAA GAAGAATACG TTCACTATAT TGAAAAACCT AAAGTCCACG AAGATAATGT	120
ATATTATAAT TTCAAAGAAT TAGTGGAAGC TATTCAAAC GATCCTTCAA AAGAATATCG	180
TCTGGGACAA TCAATGAGCG CTAGAAATGT TGTTCCTAAT GGAAAATCAT ATATCACTAA	240
AGAATTCACA GGAAACTTT TAAGTTCCTGA AGGAAAACAA TTTGCTATTA CTGAATTGGA	300
ACATCCATTA TTTAATGTGA TAACAAACGC AACGATAAAT AATGTGAATT TTGAAAATGT	360
AGAGATAGAA CGTTCTGGTC AAGATAATAT TGCATCATTG GCCAATACTA TGAAAGGTTC	420
TTCAGTTATT ACAAATGTCA AAATTACAGG CACACTTTCA GGTCGTAATA ATGTTGCTGG	480
ATTTGTAAAT AATATGAATG ATGGAACCTG TATTGAAAAT GTTGCTTTCT TTGGCAAACCT	540
ACACTCTACA AGTGGAATG GCTCTCATA AGGGGGAATT GCAGGTACAA ACTATAGAGG	600
AATTGTTAGA AAAGCATATG TTGATGCTAC TATTACAGGA AACAAAACAC GCGCCAGCTT	660
GTTAGTTCCT AAAGTAGATT ATGGATTAAC TCTAGACCAT CTTATTGGTA CAAAAGCTCT	720
CCTAACTGAG TCGGTTGTAA AAGGTAAAAT AGATGTTTCA AATCCAGTAG AAGTTGGAGC	780
AATAGCAAGT AAGACTTGGC CTGTAGGTAC GGTAAGTAAT TCTGTCAGCT ATGCTAAGAT	840
TATCCGTGGA GAGGAGTTAT TCGGCTCTAA CGACGTTGAT GATTCTGATT ATGCTAGTGC	900
TCATATAAAA GATTTATATG CGGTAGAGGG ATATTCGTCA GGTAATAGAT CATTTAGGAA	960
ATCTAAAACA TTTACTAAAT TAACTAAAGA ACAAGCTGAT GCTAAAGTTA CTACTTTCAA	1020
TATTACTGCT GATAAATTAG AAAGTGATCT ATCTCCTCTT GCAAACTTA ATGAAGAAAA	1080
AGCCTATTCT AGTATTCAAG ATTATAACGC TGAATATAAC CAAGCCTATA AAAATCTTGA	1140
AAAATTAATA CCATTCTACA ATAAAGATTA TATTGTATAT CAAGGTAATA AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260
TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320
TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380
TGACTIONAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440
TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500
AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560
CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620
TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680
AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740
TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800
ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860
CGACGCATTC GGTCAAGTA 1879

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
	50					55					60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
65					70					75					80
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85						90					95	
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
		100						105					110		
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
	130						135					140			

Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly
 145 150 155 160
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe
 165 170 175
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly
 180 185 190
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp
 195 200 205
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys
 210 215 220
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu
 225 230 235 240
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val
 245 250 255
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser
 260 265 270
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly
 275 280 285
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp
 290 295 300
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys
 305 310 315 320
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val
 325 330 335
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro
 340 345 350
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr
 355 360 365
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro
 370 375 380
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys
 385 390 395 400
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn
 405 410 415
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val
 420 425 430
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser
 435 440 445
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile
 450 455 460
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn
 465 470 475 480

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 102210"2259/60

(2) INFORMATION FOR SEQ ID NO: 221:

(A) LENGTH: 1777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTAGACAGA	TTAATTGAAA	TCGGTTCTAA	AGAGAACAAC	ATTAAAGGTT	CACGTACATT	60
CGACGCATTC	GGTCAAGTAT	TGGCTAAATA	TACTAAATCA	GGTAATTTAG	ATGCATTTTTT	120
AAATTATAAT	AGACAATTGT	TCACAAATAT	AGACAATATG	AACGATTGGT	TTATTGATGC	180
TACAGAAGAC	CATGTCTACA	TCGCAGAACG	CGCTTCTGAG	GTCGAAGAAA	TTAAAAATTC	240
TAAACATCGT	GCATTGATA	ATTTAAAACG	AAGTCACCTT	AGAAATACTA	TACTCCCACT	300
ACTGAATATT	GATAAAGCAC	ATCTTTATTT	AATTTCAAAT	TATAATGCAA	TTGCCTTTGG	360
TAGTGCAGAG	CGATTAGGTA	AAAAATCATT	AGAAGATATT	AAAGATATCG	TTAACAAAGC	420
TGCAGATGGT	TATAGAAACT	ATTATGATTT	CTGGTATCGT	CTAGCGTCTG	ATAACGTTAA	480
ACAACGACTA	CTAAGAGATG	CTGTTATTCC	TATTTGGGAA	GGTTATAACG	CTCCTGGTGG	540
ATGGGTTGAA	AAATATGGCC	GCTATAATAC	CGACAAAGTA	TATACTCCTC	TTAGAGAATT	600

CTTTGGTCCT ATGGATAAGT ATTATAATTA TAATGGAACA GGAGCTTATG CTGCTATATA 660
 TCCTAACTCT GATGATATTA GAACTGATGT AAAATATGTT CATTTAGAAA TGGTTGGTGA 720
 ATACGGTATT TCAGTTTACA CACATGAAAC AACACACGTC AACGACCGTG CGATTTACTT 780
 AGGTGGCTTT GGACACCGTG AAGGTACTGA TGCTGAAGCA TATGCTCAGG GTATGCTACA 840
 AACTCCTGTT ACTGGTAGTG GATTTGATGA GTTTGGTTCT TTAGGTATTA ATATGGTATT 900
 TAAACGCAAA AATGATGGGA ATCAGTGGTA TATTACAGAT CCAAAAACCTC TAAAAACACG 960
 AGAAGATATT AATAGATATA TGAAGGGTTA TAATGACACT TTAACCTCTC TTGATGAAAT 1020
 TGAGGCTGAA TCTGTGATTT CTCAACAAAA TAAAGATTTA AATAGTGCAT GGTTCAAAAA 1080
 AATAGATAGA GAATACCGTG ATAACAATAA ATTAAATCAA TGGGATAAAA TTCGAAATCT 1140
 AAGTCAAGAA GAGAAAAATG AATTAAATAT TCAATCTGTT AATGATTTAG TTGATCAACA 1200
 ATTAATGACT AATCGCAATC CAGGTAATGG TATCTATAAA CCCGAAGCAA TTAGCTATAA 1260
 CGATCAATCA CCTTATGTAG GTGTTAGAAT GATGACCGGT ATCTACGGAG GTAATACTAG 1320
 TAAAGGTGCT CCTGGAGCTG TTTCATTCAA ACATAATGCT TTTAGATTAT GGGGTTACTA 1380
 CGGATACGAA AATGGGTTCT TAGGTTATGC TTCAAATAAA TATAACAAC AATCTAAAC 1440
 AGATGGTGAG TCTGTTCTAA GTGATGAATA TATTATCAAG AAAATATCTA ACAATACATT 1500
 TAATACTATT GAAGAATTTA AAAAAGCTTA CTTCAAAGAA GTTAAAGATA AAGCAACGAA 1560
 AGGATTAACA ACATTCGAAG TAAATGGTTC TTCCGTTTCA TCATACGATG ATTTACTGAC 1620
 ATTGTTTAAA GAAGCTGTTA AAAAAGATGC CGAAACTCTT AAACAAGAAG CAAACGGTAA 1680
 TAAAACAGTA TCTATGAATA ATACAGTTAA ATTAAAAGAA GCTGTTTATA AGAAACTTCT 1740
 TCAACAAACA AATAGCTTTA AAACCTCAAT CTTTAAA 1777

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly
 1 5 10 15

Ser Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys
 20 25 30

Ser Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr
 35 40 45

Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His

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60

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser
 65 70 75 80
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr
 85 90 95
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser
 100 105 110
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys
 115 120 125
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr
 130 135 140
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys
 145 150 155 160
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn
 165 170 175
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys
 180 185 190
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr
 195 200 205
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp
 210 215 220
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu
 225 230 235 240
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg
 245 250 255
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu
 260 265 270
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe
 275 280 285
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn
 290 295 300
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg
 305 310 315 320
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu
 325 330 335
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp
 340 345 350
 Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn
 355 360 365
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu
 370 375 380
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln

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385		390		395		400
Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala						
	405			410		415
Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr						
	420			425		430
Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser						
	435			440		445
Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn						
	450			455		460
Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr						
	465			470		475
Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser						
	485			490		495
Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys						
	500			505		510
Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn						
	515			520		525
Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu						
	530			535		540
Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn						
	545			550		555
Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr						
	565			570		575
Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys						
	580			585		590

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTTTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGGAATTTA ATCACAGATT TAAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC	300
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
 1 5 10 15
 Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
 20 25 30
 Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
 35 40 45
 Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
 50 55 60
 Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
 65 70 75 80
 Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
 85 90 95
 Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
 100 105 110
 Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
 115 120 125
 Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
 130 135 140
 Leu Asp Lys Leu Ile Glu Glu Ala Leu
 145 150

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC 60
 AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT 120
 CGAAGTTTTA AAGGCAGTAG ATGAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC 180

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CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360
 TAAAACAACA CAAGAGGATA CCGGAACCTC TAACGCTCAA TTCATCAATA ACTGGAATCA 420
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG 720
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys	Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	1	5	10	15
Val	Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	20	25	30	
Gly	Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	35	40	45	
Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	50	55	60	
Ile	Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	65	70	75	80
Leu	Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	85	90	95	
Ile	Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	100	105	110	
Thr	Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	115	120	125	
Thr	Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	130	135	140	
Asn	Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	145	150	155	160

Leu Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val
 165 170 175

Ser Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val
 180 185 190

Asp Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser
 195 200 205

Asp Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu
 210 215 220

Tyr Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly
 225 230 235 240

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln
 245 250

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

09765272 012201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCTGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

32

32

(D) TOPOLOGY: linear

45

45

(D) TOPOLOGY: linear

33

33

(D) TOPOLOGY: linear

35

35

(D) TOPOLOGY: linear

32

32

(2) INFORMATION FOR SEQ ID NO: 239:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTCAAGATCT CTCCAACATAT GGTAAATCTG CGGATGG

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

0976527204330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

41

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

34

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

37

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

36

(2) INFORMATION FOR SEQ ID NO: 253:

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

(2) INFORMATION FOR SEQ ID NO: 254:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

31

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

(2) INFORMATION FOR SEQ ID NO: 255:

(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

38

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

(2) INFORMATION FOR SEQ ID NO: 256:

(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

37

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACCTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAACCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

006527 01300

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCACCTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

09765272 012304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTGT CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC

37

(2) INFORMATION FOR SEQ ID NO: 284:

T02270"2259460

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

09765272 012201
T02210 2259/50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTTA AATTGACTAT GCGCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTAT GAACTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

097533 0430

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTGGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

09765272.042204

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTA CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTACTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC__

37

(2) INFORMATION FOR SEQ ID NO: 311:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

00765273 012204

34

34

(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

34

34

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

30

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

31

31

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

29

29

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTGCGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTGTCTT TGGGTATTTTC GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCAGTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

09765272.012301

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

09765272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

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(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 35 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

09633 0301

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

38

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

34

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

32

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TGACCTGCAG ACGATTTTTG AAAAATGGAG GTGTATC

37

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTGTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

T022T0"2269/60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAAAC TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

09765372.042204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AAACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

09622 01204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTCTGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTTC TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGTACCAG CAACAAAGCG AGCAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0965372.013304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

096537 013904

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

T02270"22252460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGG -

47

(2) INFORMATION FOR SEQ ID NO: 392:

0976532 04304

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAACT GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACTGGATCC AGTAAATGCG CAATCAAATT C

31

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

AGTCCTGCAG GTATTTAGCC CAATAATCTA TAAAGCT

37

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

CAGTGGATCC TTACCGCGTT CATCAAGATG TC

32

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

GACTAAGCTT GCCAGATGTT GAAAAGAGAG TG

32

(2) INFORMATION FOR SEQ ID NO: 405:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCG

40

(2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTCCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

0965273 012201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTTTAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTCGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0076537.043001

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

09765272.042004

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(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTTT CAATATTTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTTCAGGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

0976527.012204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

0976527.042204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GA CTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GA CTGTGCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CA GTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GA CTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AG TCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

09765272 042204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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